

**REMARKS**

Reconsideration and withdrawal of the objections and rejections to the application are requested in view of the amendments and remarks presented herein, which place the application into condition for allowance. The Examiner is thanked for his helpful suggestions regarding claim amendments, and for indicating that claim 18 would be allowable if rewritten in independent form.

**I. STATUS OF THE CLAIMS AND FORMAL MATTERS**

Claims 1 and 3-16 are pending in this application. Claims 1, 13, and 14 are amended; claims 2, 17, and 18 are canceled. Applicants reserve the right to file divisional applications to pursue the full scope of the claims.

No new matter has been added by these amendments. Support can be found throughout the specification. Specifically, support for the amendment to claim 1 can be found in canceled claim 17.

It is submitted that these claims are patentably distinct from the references cited by the Examiner, and that these claims are in full compliance with the requirements of 35 U.S.C. §112. The amendments of the claims herein are not made for the purpose of patentability within the meaning of 35 U.S.C. §§ 101, 102, 103 or 112; but rather the amendments are made simply for clarification and to round out the scope of protection to which Applicants are entitled. Furthermore, it is explicitly stated that the herewith amendments should not give rise to any estoppel, as the herewith amendments are not narrowing amendments.

**II. THE REJECTIONS UNDER 35 U.S.C. §112, 1<sup>ST</sup> PARAGRAPH, ARE OVERCOME**

**The Specification Contains Adequate Written Description**

Claims 1-17 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking adequate written description for the broad class of any and all DNAs with caryopsis-specific promoter activity and having the indicated similarity to the disclosed sequence. The Office Action contends that nucleic acid sequences having as little as 75% identity “embraces widely variant species that cannot be described by disclosing only one species within the genus”. Claim 1 has been amended to recite sequence identity of 90–99%.

The Examiner is respectfully asked to reconsider his position with respect to the percent identity issue, and in doing so, his attention is drawn to Example 14 of the USPTO’s “Synopsis of Application of Written Description Guidelines”. Example 14 presents a fact pattern that is

analogous with that of the instant application. The claim in Example 14 recites the structure of the claimed protein, in the form of a SEQ ID NO and variants with a particular percent identity to the recited sequence, and function in the form of identifying the reaction that the protein catalyzes (i.e. its enzymatic activity). Claim 1 of the instant application recites (1) structure of the claimed protein in the form of a SEQ ID NO, and variants with 90-99% identity to the recited sequence, and (2) function of the claimed protein in the form of its caryopsis-specific promoting activity. As discussed in Example 14, even if the claimed SEQ ID NO is the only species disclosed, it is representative of the genus because all members of the genus have the claimed level of identity with and function of the protein described by the reference sequence. Therefore, according to Example 14 of the Written Description Guidelines, claim 1, as presented herein, meets the written description requirement of 35 U.S.C. §112, first paragraph.

The Office Action makes several allegations, among them that the group of sequences having 90-99% identity with one of the nucleic acid sequences stated under a) embraces “widely variant species” and that the art is unpredictable. Further, the “relevant identifying characteristics” of the species are clearly stated in the claims: the claimed molecule can be identified by its caryopsis-specific promoting activity and by its sequence, as discussed above. According to MPEP 2163.04, “[a] description as filed is presumed to be adequate, unless or until sufficient evidence or reasoning to the contrary has been presented by the examiner to rebut the presumption.” No such evidence has been presented here. Contrary to the guidelines mandated by MPEP 2163.04(I), a *prima facie* case providing reasons why the skilled artisan would not have recognized that the inventors possessed the invention, as claimed, at the time of filing has not been made in this instance.

### **The Claims Are Enabled**

Claims 14 and 16 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking enablement. The rejection is traversed.

The Office Action indicates on page 6 that the arguments set forth in the Response of February 26, 2003 were not persuasive, as they failed to account for the scope of the claimed subject matter. It was argued that it would require undue experimentation to practice the full scope of the invention as claimed, as the skilled artisan would have to engage in trial and error experimentation to identify an effective inhibitory antisense or ribozyme molecule for each and every gene expressed in the caryopsis.

The Applicants have demonstrated that the promoter of the invention can provide tissue-specific expression, i.e. is a caryopsis-specific promoter. It can be used to express nucleic acids that are functionally linked to the promoter sequence, such as in an expression cassette or vector. The nucleic acid that is linked to the promoter can be a polypeptide-encoding sequence (e.g. a gene), and can be linked to the promoter in sense or antisense orientation. The nucleic acid may also encode a non-translatable RNA, such as an anti-sense RNA or a ribozyme. As the promoter of the present invention is specifically active in the caryopsis of plants, it is clear to a person skilled in the art that it can be used for caryopsis-specific expression of ribozymes or antisense RNA. As a consequence, the effect of the expression of ribozyme or antisense RNA is also focused on the respective tissue where the promoter is active.

It is well known in the art that plant systems exhibit a phenomenon known as "homology-dependent gene silencing". This phenomenon is based on the observation that plants possess a transient pairing mechanism of homologous sequences, which induces the methylation of often multiple genes containing these homologous sequences. An increase in DNA methylation frequently accompanies inactivation of genes, and is a well-known mechanism of gene silencing. Researchers in an attempt to express foreign DNA in plants, found that transgenes were often inactivated by this phenomenon.

The Examiner is respectfully directed to page 5, lines 22-31, and continuing on page 6 of the instant application, where the phenomenon of homology-dependent gene silencing, which is also known in the art as "co-suppression", that can be advantageously applied by means of promoter sequences, is discussed. It is clearly pointed out that "co-suppression strategies using promoters have been described in detail by Vaucheret et al." A reference by Matzke et al, which also discusses co-suppression of plant genes, is further discussed.

Preferred embodiments of the present invention describe suppression of caryopsis-specific genes using tissue- and developmentally-specific promoters of the present invention. The Applicants appreciate the Examiner's argument that it would require undue experimentation to create antisense sequences to every caryopsis-specific gene; however, it is respectfully pointed out that, while antisense nucleic acids comprising sequences homologous to structural genes can be synthesized and operably linked to the promoters of the present invention, expression of the promoter sequence itself, positioned in the antisense orientation and operably linked to the

promoter sequences in the sense orientation, would produce a similar, if not identical effect of caryopsis-specific gene suppression.

If inactivation of known caryopsis-specific genes is desired, antisense and ribozyme sequences could easily be designed according to methods well known in the art. The Examiner is respectfully invited to review the hundreds of references detailing the practice of gene suppression by antisense technology (a representative list of publications is enclosed). Similarly, it is well within the purview of the skilled artisan to design a ribozyme that preferentially cleaves any sequence that contains the promoter sequences of the present invention. Therefore, in this scenario, it would not require trial and error experimentation to practice the full scope of the invention as claimed.

In view of the amendments and arguments presented, it is believed that the rejections under 35 U.S.C. §112, first paragraph, are overcome, and reconsideration and withdrawal are requested.

### **III. THE REJECTIONS UNDER 35 U.S.C. §112, 2<sup>ND</sup> PARAGRAPH, ARE OVERCOME**

Claims 2, 13 and 14 were rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which the Applicants regards as the invention. Claim 2 has been canceled, obviating the rejection with respect to it.

Claim 13 has been amended to recite "in caryopses", as suggested by the Examiner.

Claim 14 has been amended to clarify that it is the nucleic acid under the control of the caryopsis-specific promoter that is suppressive.

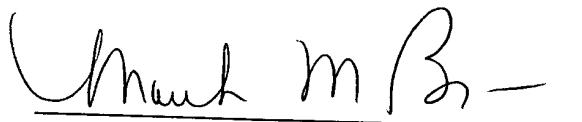
In view of these amendments, reconsideration and withdrawal of the rejections under 35 U.S.C. §112, second paragraph, are requested.

CONCLUSION

Applicants believe that the application is now in condition for allowance. Favorable reconsideration of the application and prompt issuance of a Notice of Allowance are earnestly solicited.

Respectfully submitted,  
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A		C		D		E		F		G		H		I	
1 Overview of reported anti-sense cases (entries complete up to 1999, nearly complete 2000, incomplete 2001, last entry November 2001)															
2	Target gene	Gene function	Major expression	Deficiency phenotype	Silencing method	Target species	gene source	fragment length of insert					Reference	TECH CENTER	1600/2000
3	Inducible														
4	aspartate amino transferase-P2 (ACE1)	?	upon Cu induction	decreased enzyme activity and decreased nodule asparagine concentration	pACE1 (Cu-inducible)-antisense	<i>Lotus corniculatus</i>	?						Melt et al. (1996) Transgenic Research 5(2), 105-113		
5	Aox 1a (alternative oxidase)	terminal electron acceptor of the alternative pathway in the electron transport chain	upon Cu induction	effective cytochrome pathway inhibition (production of up to 8.8 times more ethanol via aerobic fermentation)	MRE (Cu-inducible)-antisense	<i>Arabidopsis thaliana</i> cv. Columbia	<i>Arabidopsis thaliana</i> (L.) Heynh	cDNA (+/- 1kb)					Potter FJ et al. (2001) <i>Planta</i> 212, 215-221		
6	Cak1At	cyclin-dependent kinase-activating kinase: role in the differentiation of initial cells (but independent of cell division)	upon glucocorticoid induction (DEX)	gradual reduction of CDK activity; inhibition of root growth; transcript reduction upon induction	pGVG-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	Cak1At coding region					Umeda M et al. (2000) <i>Proc Natl Acad Sci USA</i> 97(24) 13396-13400		
7	cdc2b	kinase-related protein (cell cycle)		short hypocotyl and open-cotyledon phenotype	inducible a.s.	<i>Arabidopsis thaliana</i> L.							Yoshizumi et al (1999) <i>Plant Cell</i> 11, 1883-1895		
8	GUS (beta-glucuronidase: uidA)	beta-glucuronidase enzyme	upon T7-polymerase induction (crossing)	loss of blue staining	pT7-sense	tobacco ( <i>Nicotiana tabacum</i> L.)	<i>Escherichia coli</i>						Zeitouni S et al. (1999) <i>Plant Science</i> 141(1) p59		
9	Hsp70 (heat shock protein)	protective role in thermotolerance	upon heat stress	downregulation of hsp70 genes	soybean heat-inducible PGmhsp17.6-L-antisense	<i>Arabidopsis thaliana</i> L. cv. Columbia	<i>Nicotiana tabacum</i> L. (X63106)	cDNA fragment (1667bp)					Lee JH and Schoff F (1996) <i>Mol Gen Genet</i> 252(1-2): 11-19		
10	le 20	drought-induced putative histone H1			inducible a.s.	tomato							not successful		
11	NDP-kinase	guanine nucleotide synthesis?	upon heat stress	inhibition of cell elongation in coleoptile	pHPB81-antisense	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)	cDNA-fragment (about 0.7kb)					Pan L. et al. (2000) <i>Plant Physiology</i> 122, 447-452		
12	PPO (protoporphyrinogen oxidase)	last common enzyme of the biosynthesis of the heme group and chlorophyll	after crossing with plant expressing constitutive GAL4-C1 chimeric transgene	growth alterations and necrotic lesions (similar to pathogen-induced hypersensitive reaction SAR) on leaves	GAL 4/UAS-antisense-35S terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment: 857bp					Molina A et al. (1999) <i>Plant J</i> 17(6), 667-678		
13	SAMDC (S-Adenosylmethionine decarboxylase; EC 4.1.1.50)	biosynthesis of the polyamines spermidine and spermine	increase of SAMDC activity during the early stages of polymerisation	decrease in SAMDC transcript level, SAMDC activity and total polyamine levels	patatin promoter antisense or sense (pBIN19); p35S(2x)-antisense-i35S or tetr inducible pro-antisense tocs	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	cDNA fragment (1800bp? ?)					Kumar A et al. (1996) <i>Plant J</i> 9(2), 147-158;		
14	Wak1 (cell wall associated receptor kinase: pro25; LO4998)	a pathogen related (PR) protein	induced by pathogen infection (and by INA or SA)	bleaching and death upon induction; but no notable influence on mRNA?...	pPR1-antisense-tm1 terminator (INA inducible promoter)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length cDNA (2.1kb??)					He ZH et al. (1998) <i>Plant J</i> 14(1), 55-63		
15	Wak4 (cell wall associated receptor kinase)	possible vital role of WAKs in cell elongation and required for plant development	mainly in green organs	significant decrease of WAK proteins: undetectable after 96h after induction: impaired cell elongation and blocked lateral root development	6XUAS GAL4ind pro-antisense-? terminator (dexamethosone inducible; pTA7002)	<i>Arabidopsis thaliana</i> L. ec. Columbia	<i>Arabidopsis thaliana</i> L.	full-length genomic fragment (2.4kb??)					Lally D et al. (2001) <i>The Plant Cell</i> 13(), 1317-1331		
16	Natural														
17	atp6	role in cytoplasmic-male-sterility (CMS); energy metabolism	expressed by the mitochondrial genome	CMS	2 antisense transcripts (pseudogene)	<i>Oryza sativa</i> (cybrids)	<i>Oryza sativa</i> (cybrids)	2 different a.s. transcripts (2.2 and 2.6 bp long)					Akagi H et al. (1994) <i>Curr Genet</i> 25(1), 52-58		
18	chs (nilva locus)	pigment biosynthesis	flower tissue	loss of flower colour	sense/antisense? = "Inverted duplication"	<i>Anthirrhinum majus</i> (= gene rearrangement)	<i>Anthirrhinum majus</i> (= gene rearrangement)	Inverted duplication in promoter region					Bollmann et al. (1991) <i>The Plant Cell</i> 3, 1327-1336, Lister et al. (1993) <i>The Plant Cell</i> 5, 1541-1553; Lister and Martin (1989) <i>Genetics</i> 123(2), 417-425; Coen and Carpenter (1988) 7(4), 877-883		
19	PAI	tryptophan biosynthesis	ubiquitous	fluorescent phenotype	sense/antisense? = duplication-tail to tail inversion	<i>Arabidopsis thaliana</i> L. ec. Wassilewskija	<i>Arabidopsis thaliana</i> L. (gene duplication)	tail to tail rearrangement					Martenssen R. (1996) <i>Current Biology</i> 6(7), 810-813 (see b-gene); Bender and Fink (1995) <i>Cell</i> 83, 725-734; Jeddeloh et al. (1998) <i>Genes and Development</i> 12, 1714-1725; Melquist et al. (1999) <i>Genetics</i> 153(1), 401-13		
20	S-genes	control of pollen-stigma self-incompatibility	developing silks	self incompatibility?	antisense	Brassica							Ansalid R et al. (2000) <i>J Biol Chem</i> 275(31), 24146-24155		
21	r-gene (red locus)	transcription factor	seeds	altered seed coloration	sense (R-st), antisense (R-r)	maize ( <i>Zea mays</i> )	maize ( <i>Zea mays</i> )	rearrangement					Eggleson et al. (1995) <i>Genetics</i> 141(1), 347-360; Ronchi et al. (1995) <i>Embo J</i> 14(21), 5318-5328; Martenssen R. (1996) <i>Current Biology</i> 6(7), 810-813		
22	silencing of transgenes														
23	chimeric atp9; unedited (ATP-synthase subunit 9)	role in male sterility	transgene targeted to mitochondria; expression of the transgene in vegetative and generative tissue	restoration of male fertility	p35S-antisense yeast precoxIV-CaMV termIV	tobacco ( <i>Nicotiana tabacum</i> L.)	wheat	entire coding sequence of the unedited coding sequence					Zabaleta E et al. (1996) <i>Proc Natl Acad Sci USA</i> 93(20), 11259-11263		
24	bar	herbicide resistance	?	loss of herbicide resistance	pUB1-chimeric sense construct	rice ( <i>Oryza sativa</i> L.)							Kumpatla SP et al. (1997) <i>Plant Physiol</i> 115(2), 361-371; Kumpatla SP and Hall TC (1998) <i>Plant J</i> 14(1), 129-135; Kumpatla SP and Hall TC (1999) <i>IUBMB Life</i> 40(4), 459-467		

	A	B	C	D	E	F	G	H	I
25	CAT (chloramphenicol acetyltransferase)	transgenic reporter gene	constitutive (35S)	loss of CAT activity	p35S-antisense	carrot protoplasts	bacterial TrN9 transposon		Ecker JR and Davis RW (1986) Proc Natl Acad Sci USA 83(15), 5372-5376; Bourque JE and Folk WR (1992) Plant Mol Biol 19(4), 641-647
26	GUS (beta-glucuronidase; uidA)	transgenic reporter gene; (p35S-sense-nos terminator)	constitutive	reduced blue staining	p35S-antisense fragments; transient expression	Petunia hybrida protoplasts	Escherichia coli		de Lange P et al. (1993) Plant Mol Biol 23, 45-55
27	GUS (beta-glucuronidase; uidA)	beta-glucuronidase enzyme	constitutive (p35S-sense-)	reduced blue staining	pca/antisense T7	tobacco ( <i>Nicotiana tabacum</i> L.)	Escherichia coli	41bp	Cannon M et al. (1990) Plant Mol Biol 15, 39-47
28	GUS (beta-glucuronidase; uidA)	beta-glucuronidase enzyme		reduced blue staining	seed specific promoter-antisense-	tobacco ( <i>Nicotiana tabacum</i> L.)	Escherichia coli		Fujiwara et al. (1992) Plant Mol Biol 20, 1059-1069
29	GUS (beta-glucuronidase; uidA)	beta-glucuronidase enzyme		reduced blue staining			Escherichia coli		Depicker group
30	GUS (pollen)	Gus expression in pollen, leaves and roots	pollen, leaves and roots	significant reduction in pollen GUS activity	pLAT52-antisense-nos	tobacco	Escherichia coli	?	Wilkinson et al (1998) J. Exp. Bot. 49, 1481-1490
31	hpt (hygromycin phosphotransferase e) and NIR (nitrite reductase)	antibiotic resistance and nitrate biosynthesis	?	Silencing of hpt and endogenous NIR-gene: promoter mediated; chlorosis	p35S-hguro and p35S-RIN (antisense)	tobacco			Park YD et al. (1996) Plant J 9(2), 183-194
32	hygR and kanaR genes driven by various promoters	resistance to antibiotic	depending on the promoter	loss of resistance		tobacco			multiple papers by the Matzke group. Original (?) : Matzke et al (1998) EMBO J 8, 643-649
33	aleurone-specific Ltp2-GUS	lipid transfer protein?	seeds	specific GUS staining pattern on seeds	partial antisense	rice			Morino et al (1999) Plant Journal 17, 275-285
34	NOS gene	Nopaline synthase	constitutive	Loss of nopaline accumulation	p35S-sense-; p35S-antisense nos ter	tobacco ( <i>Nicotiana tabacum</i> L.)	Agrobacterium (T-DNA) 5'DNA fragment		Rothstein SJ et al. (1987) Proc Natl Acad Sci USA 84(23), 8439-8443; Gorling et al (1991) PNAS 88, 1770-1774; Fujiwara et al (1993) Plant Cell Reports 12, 133-138
35	npt II (neomycin phosphotransferase II)	resistance to aminoglycoside antibiotics	?	reduction of transcript	sense and antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	bacterial TrN5 transposon		Depicker group; Van Houdt H et al. (2000) 263(3), 995-1002
36	p35s-RoIC		constitutive	rescue the roIC-induced male sterility	p35S-antisense	P35S-roIC transformed tobacco ( <i>Nicotiana tabacum</i> L. plants)	Agrobacterium rhizogenes roIC fragments : 192bp and 968bp		Schmülling T et al. (1993) Mol Gen Genet 237, 385-394; Schmülling T and Röhrlig H (1995) Mol Gen Genet 249, 375-390
37	PR-glucanase (pathogenesis-related beta-1,3-glucanase)	male sterility due to beta-1,3-glucanase activity	tapetum specific expression of the transgene by A.t. A9 and A3 promoters	restoration of male fertility	pA9 and pA3 + antisense sequences	tobacco			Hird DL et al. (2000) Transgenic Res 9(2), 91-102
38	Waterhouse:								
39	chs	pigment biosynthesis			ihp, sense, a.s.	Arabidopsis			
40	delta 12	fatty acid biosynthesis			ihp, hp, a.s.	cotton			
41	delta 9	fatty acid biosynthesis			ihp, hp, a.s.	cotton			
42	delta12	fatty acid biosynthesis			ihp, hp, sense, a.s.	Arabidopsis			
43	fic	flowering time regulator			ihp, a.s.	Arabidopsis			
44	virus (PVY)				ihp, hp, sense, a.s.	tobacco			
45	Other								
46	A9 (tapetum-specific)	not known (not essential for male fertility...)	tapetum (buds)	very low or undetectable levels of A9 mRNA	Arabidopsis A9 promoter - antisense-	Brassica napus	Brassica napus cv Westar	full-length (490 bp)	Turgut K et al. (1994) Plant Mol Biol 24(1), 97-104
47	ABA2 (zeaxanthin epoxidase)	abscisic acid biosynthesis	?	rapid seed germination and reduction of Abscisic acid (ABA)-abundance in seeds	p35S+duplicate d enhancer domain)-antisense-rbcS3' region	<i>Nicotiana plumbaginifolia</i> a	<i>Nicotiana plumbaginifolia</i> a	ABA2 fragments : 0.8kb and 1.4 kb	Frey A et al. (1999) Plant Mol Biol 39(6), 1267-1274
48	Le-ACC2 synthase	biosynthetic pathway of ethylene	during fruit ripening	inhibition of fruit ripening	p35S-antisense nos terminator;	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L.)	full-length (1789 bp)	Oeller et al. (1991) Science 254, 437-439
49	Le-ACC2 synthase	biosynthetic pathway of ethylene	during fruit ripening	inhibition of fruit ripening	p35S-sense-(?); p35S-antisense ; pE8-antisense	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L.)		Theologis et al. (1993) Dev Genet 14(4), 282-295
50	ACC oxidase (MEL1)	ethylene biosynthesis	all green tissue; inducible by chx and wounding	late fruit ripening	p35S-MEL1 antisense-T7-5	melon ( <i>Cucumis melo reticulatus</i> Naud. Cv. Védrantais)	melon ( <i>Cucumis melo reticulatus</i> Naud. Cv. Védrantais)	full-length (1.2kb)	Ayub R et al. (1996) Nat Biotechnol 14(7), 862-866
51	ACC oxidase (pTOM3)	ethylene biosynthesis	in leaves and ripening fruit	late fruit ripening	p35S-antisense 35S terminator	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L.)	fragment (1.1 kb)	Hamilton et al (1990) Nature 346, 284-287; Schuch W (1991) Symp Soc Exp Biol 45, 117-127; Lycett GW (2000) Methods Mol Biol 141, 145-155
52	ACC oxidase (ACO1)	ethylene biosynthesis	all green tissue; inducible by chx and wounding	late fruit ripening; strong improvement in silencing when tandem repeat was used	co-suppression (35S-sense-) + 35S-short tandem repeat sense_antisense + sense-	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L. cv. Ailsa Craig)	ful length and full length + short repeats (in tandem: sense + antisense)	Hamilton et al (1998) Plant J. 15, 737-746
53	ACC oxidase and/or ACC synthase	ethylene biosynthesis	upon wounding	reduction of inducible ethylene production	p35S-antisense ; p35S-'Incomplete' sense-	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)		Knoester M et al. (1997) Plant Science 126(2), 173-183

	A	B	C	D	E	F	G	H	I
54	ACL5 (Acualis5)	key enzyme in the polyamine biosynthesis pathway (spermine synthase)	?	reduction in the length of stem internodes	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length	Hanzawa Y et al. (2000) EMBO J 19(16), 4248-4258
55	ALACX1 and 2 (Long-chain acyl-CoA oxidase)	peroxisomal fatty acid beta-oxidation: mobilization of storage lipids	seedlings and mature tissues	reduced root growth; only ACX1 transcript could be reduced by antisense technology	p35S+ dual enhancer-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	partial cDNA clones	Hooks MA et al. (1999) Plant J 20(1), 1-13
56	ADC (arginine decarboxylase)	Involved in the early steps of the polyamine biosynthesis	?	down regulation of the activity of endogenous arginine and ornithine decarboxylases; marked decrease in the level of putrescine and spermidine	p35S(+ duplicated enhancer sequence)-adc antisense-35S terminator	rice ( <i>Oryza sativa</i> L. cv. ITA 212)	oat	full-length (2124 bp)	Capell et al. (2000) Mol Gen Genet 264, 470-476
57	Adh2 (antisense orientation)	enzyme involved in ethanol fermentation	upon anaerobic induction (in roots?)	65% ADH activity and 25% decrease in ethanol production in anaerobic roots	p7-antisense-	cotton ( <i>Gossypium hirsutum</i> L.)	cotton ( <i>Gossypium hirsutum</i> L.)?		Ellis MH et al. (2000) Aust J Plant Physiol 27, 1041-1050
58	ADP-glucose pyrophosphorylase (AGPase)	carbon metabolism; starch biosynthesis	tuber	influence on tuber formation and abolition of starch formation: decrease in dry matter;	p35S-antisenseocs terminator	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	potato ( <i>Solanum tuberosum</i> L.)	fragment of subunit B (1.6kb -85% of full-length)	Möller-Röber B et al. (1992) EMBO J 11, 1229-1238; Röber M et al. (1996) Planta 199(4), 528-536; Loyd JR et al. (1999) Planta 209(2), 230-238; Geigenberger P et al. (1999) Planta 209(3), 338-345
59	ViAGPC (ADP-glucose pp-lyase)	carbon metabolism; starch biosynthesis	cotyledons	moderate decrease in starch and increase in sucrose content	seed-specific legumin B4 promoter (pLeB4)-antisense-	<i>Vicia narbonensis</i>	<i>Vicia faba</i>	full-length	Weber et al. (2000) Plant J 24(1), 33-43
60	agamous (AG: ATG1)	floral identity gene	flowers	flower aberration: whole range of aberrations	p35S-sense- (Co-suppression); p35S-antisense-	<i>Arabidopsis thaliana</i> L.)	<i>Arabidopsis thaliana</i> L.)	fragments	Mizucami Y and Ma H (1992) Cell 71, 119-131; Mizucami Y and Ma H (1995) Plant Mol Biol 28, 767-784
61	agamous (ag) and clavata 3 and apetala 1 and perianthia	floral identity genes	flowers	flower aberration	dsRNAi = p35S-sense + GUS-loop + antisense-	<i>Arabidopsis thaliana</i> L.)	<i>Arabidopsis thaliana</i> L.)	fragments	Chuang and Meyerowitz (2000) Proc. Natl. Acad. Sci. 97(9), 4985-4990
62	AGAMOUS (TAG1)	floral identity gene; expressed in stamens and carpels	flowers	floral aberration; sense TAG1 RNA not detectable but antisense transcript detectable in transgenic plants	p7-antisense-	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L.)	?	Pruell L et al. (1994) Plant Cell 6(2), 163-173
63	AGL20 (MADS-box gene)	control of flowering	flowers	delay in flowering time	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	fragment (without MADS-box)	Bonhomme F et al. (2000) Plant J 24(1), 103-111
64	AKR-gene	chloroplast differentiation	green tissues; light dependant expression	chlorosis; reduces seed production	p35S-sense or antisense-nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	fragment (1051bp)	Zhang H et al. (1992) Plant Cell 4(12), 1575-1588
65	Aifin1	transcriptional regulator in plants		enhanced sensitivity to NaCl inhibition	p35S-antisense	alfalfa ( <i>Medicago sativa</i> L.)	alfalfa ( <i>Medicago sativa</i> L.)	fragment (904bp)	Winicov I and Bastola DR (1999) Plant Physiol 120(2), 473-480
66	AOX (alternative oxidase - aox1)	alternative pathway to decrease the formation of reactive oxygen species (ROS)	Overall: mitochondrion	altered growth and metabolism under P-limitation; impaired cell growth and decrease in efficiency of carbon utilization	p35S-sense-T7 terminator; p35S-antisense-T7 terminator	cultured tobacco cells ( <i>Nicotiana tabacum</i> L. cv. Petit Havana SR1)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length	Vanlerberghe GC et al. (1994) Plant Physiol 106, 1503-1510; Vanlerberghe GC et al. (1997) Plant Physiol 113, 657-661; Parsons HL et al. (1999) Plant Physiol 121(4), 1309-1320
67	AOX (alternative oxidase)	alternative pathway to decrease the formation of reactive oxygen species (ROS)	Overall: mitochondrion	cells with a significantly higher level of ROS	p35S-antisense T7 terminator	cultured (AS8) tobacco cells ( <i>Nicotiana tabacum</i> L. cv. Petit Havana SR1)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length	Maxwell DP et al. (1999) Proc Natl Acad Sci USA 96(14), 8271-8276
68	APX (ascorbate peroxidase) or CAT (catalase)	reactive oxygen intermediates (ROI)-detoxifying enzymes	upon ozon induction	increased susceptibility to ozon injury; hyperresponsible to pathogen attack	p7(in pB121 vector)-antisense APX; p35S-antisense CAT-	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L. cv. Xanthi)	fragment (338bp; 45% from full-length)	Orvar BL and Ellis BE (1997) Plant J 11(6), 1297-1305; Mittler et al. (1999) Proc Natl Acad Sci USA 96(24), 14165-14170
69	ARC1	Implicated in the self-incompatibility response	stigma	partial breakdown of self-incompatibility; decrease in transcript levels	pSLR1 (target to the stigma)-antisense-	<i>Brassica napus</i> W1	<i>Brassica napus</i>	full-length	Stone SL et al. (1999) Science 286(5445), 1729-31
70	beta-glucanase	glucan degradation		reduced enzymes, mRNA	sense gene	tobacco			Van Montagu lab
71	Bcp1	gene required for male fertility	active in both diploid tapetum and haploid microspores	male infertility: failure to produce elongated siliques and seeds (16 out of 42 primary transformants)	pBcp1-antisense-; pLAT52-antisense-; p35S-antisense nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	coding region (500bp);	Xu H et al. (1995) Proc Natl Acad Sci USA 92(6), 2106-2110; Luo H et al. (2000) Plant J 23(3), 423-430
72	BIP (lumen binding protein; BLP4-isofrom)	role in the transport and secretion of proteins	tissues with high rates of cell division, secretory tissues	not successful: deleterious for cell viability	p35S-antisense nos terminator	tobacco ( <i>Nicotiana tabacum</i> L.) and BY2 cell cultures	tobacco ( <i>Nicotiana tabacum</i> L.)	?	Leborgne-Castel N et al. (1999) Plant Cell 11(3), 459-469
73	OsBRI1 (a putative brassinosteroid receptor kinase - d61 gene)	Brassinosteroid perception	vegetative shoot apices	dwarfism	p35S-antisense nos terminator	<i>Oryza sativa</i> cv. Nipponbare	<i>Oryza sativa</i> cv. Nipponbare	full-length	Yamamoto C et al. (2000) Plant Cell 12(9), 1591-1606
74	BSH (SNF5-type protein)	a component of an At SWI/SNF-complex: SNF5-type protein	ubiquitous	bushy growth and seedless flowers	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length	Brzeski J et al. (1999) Nucleic acid res 27(11), 2393-2399
75	2CP (2-cysteine peroxiredoxin)	role in plant defense mechanisms (anti-oxidant network of chloroplasts)	leaf (chloroplasts)	enhanced activity and expression of enzymes associated with ascorbate metabolism	p35S-antisense	<i>Arabidopsis thaliana</i> L.	barley	cDNA-fragment (full coding region)	Baier M and Dietz KJ (1999) Plant Physiol 119, 1407-1417; Baier M et al. (2000) Plant Physiol 124(2), 823-832

	A	B	C	D	E	F	G	H	I
76	4CL (4-coumarate: coenzyme A ligase; D43773)	lignin biosynthesis	overall?	brown coloration of the cell walls of xylem tissue; change in lignin composition	p35S-sense or antisense-Tnos	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	near full-length cDNA (full coding region; 1855bp)	Kajita S et al. (1996) <i>Plant Cell Physiol</i> 37(7), 957-965; Kajita S et al. (1997) <i>Plant Physiol</i> 114, 871-879
77	4CL (4-coumarate: coenzyme A ligase)	lignin biosynthesis	highly expressed in bolting stems (major site for lignin deposition)	decrease in the Guaiacyl/syringyl ratio; change in lignin composition	p35S-antisense nos terminator; pPC4CL (parsley 4CL1 promoters) antisense-nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	1.6/1.9 kb 4CL-fragment	Lee D et al. (1997) <i>Plant Cell</i> 9(11), 1985-1998
78	Pt4CL1 (4-coumarate:coenzyme A ligase)	lignin biosynthesis	woody tissues (xylem)	45% reduction in lignin and 15% increase in cellulose; enhanced growth	p35S(double enhancer)-antisense-	aspen ( <i>Populus tremuloides</i> Michx.)	aspen ( <i>Populus tremuloides</i> Michx.)	cDNA-fragment (full coding region)	Hu WJ et al. (1999) <i>Nat Biotechnol</i> 17(8), 808-812; Sederoff R. (1999) <i>Nat Biotechnol</i> 17(8), 750-751
79	C40.4	role in photosynthesis	leaves stem and flowers	stunted growth and decreased tuber yield	p35S-antisense nos terminator	potato ( <i>Solanum tuberosum</i> cv andigena)	potato ( <i>Solanum tuberosum</i> )	fragment (586bp)	Monte E et al. (1999) <i>Plant J</i> 19(4), 399-410
80	C4H (cinnamic acid 4-hydroxylase)	trans-cinnamic acid biosynthesis = influence on PAL activity by feedback modulation)	leaves and stems	reduced PAL activity and reduced levels of phenylpropanoid compounds	p35S-sense or antisense-nos terminator	tobacco ( <i>Nicotiana tabaccum</i> L. cv. Xanthi)	alfalfa-C4H ( <i>Medicago sativa</i> )	complete cDNA sequence	Sewalt VJH et al. (1997) <i>Plant Physiol</i> 115, 41-50; Blount JW et al. (2000) <i>Plant Physiol</i> 122(1), 107-116
81	CAD (cinnamyl-alcohol dehydrogenase)	lignin biosynthesis	all tissues (cell wall composition)	55 to 20 % reduction of CAD activity, no difference in lignin content, altered lignin composition, some transformants show brownish coloration	p35S-antisense-(pGAH binary vector)	tobacco ( <i>Nicotiana tabaccum</i> L. cv. Xanthi nc)	<i>Aralia cordata</i>	cDNA fragment (full coding region 1267bp; 70% homology)	Hibino et al. (1985) <i>Biosci Biotech Biochem</i> 59, 929-931;
82	CAD (cinnamyl-alcohol dehydrogenase)	lignin biosynthesis	all tissues (cell wall composition)	altered lignin composition and red coloration of the xylem	p35S-sense or antisense-17 terminator	poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	cDNA full length (1.4kb)	Higuchi et al. (1994) <i>J Biotechnol</i> 37, 151-158; Baucher M et al. (1996) <i>Plant Physiol</i> 112, 1479-1490
83	CAD (cinnamyl-alcohol dehydrogenase)	lignin biosynthesis	all tissues (cell wall composition)	altered lignin composition and red coloration of the stem	p35S-antisense T7 terminator or nos ter	alfalfa ( <i>Medicago sativa</i> L.)	alfalfa ( <i>Medicago sativa</i> L.)	3 different CAD fragments (0.4kb; 1.5kb and 1kb)	Halpin C et al. (1994) <i>Plant J</i> 6(3), 339-350; Baucher M et al. (1999) <i>Plant Mol Biol</i> 39(3), 437-447
84	CAD (cinnamyl-alcohol dehydrogenase; EC 1.1.1.195) and CCR	lignin monomer biosynthetic pathway	CAD is expressed in both lignified and unlignified tissues/cells	altered lignin composition	p35S-antisense nos terminator	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	1kb for CAD and 1.3kb for CCR	Ralph J et al. (1998) <i>Proc Natl Acad Sci USA</i> 95(22), 12803-12808
85	CAOMT (cafeic acid O-methyl transferase)	lignin biosynthesis	xylem?	either mottled or complete red-brown coloration in woody stems	double p35S-sense-(cosuppression)	quaking aspen ( <i>Populus tremuloides</i> Michx.)	quaking aspen ( <i>Populus tremuloides</i> Michx.)	full-length	Tsai CP et al. (1998) <i>Plant Physiol</i> 117(1), 101-112
86	CAT-1 (primary leaf catalase)	H2O2 detoxification; H2O2 scavenging enzyme	predominantly in leaves	significant increase in CO2 compensation point (decreased photospiration?) at higher temperatures (35°C)	p35S-sense or antisense-	tobacco ( <i>Nicotiana tabaccum</i> L.); <i>Nicotiana sylvestris</i> ; <i>Gossypium hirsutum</i> L.	tobacco ( <i>Nicotiana tabaccum</i> L.); <i>Nicotiana sylvestris</i> ; <i>Gossypium hirsutum</i> L.	fragments or full-length (see article p262)	Brissone LF et al. (1998) <i>Plant Physiol</i> 116, 259-269
87	Cat1 and/or Cat2 (plant catalases)	role in salicylic acid signalling; H2O2 detoxification	predominantly in leaves (Cat1 in the palisade parenchyma cells and Cat2 in the phloem)	high light conditions: induction of pathogenesis related expression without pathogenic challenge; severe leaf damage	p35S-cat2 antisense-ocs terminator; p35S(double)-sense or antisense-3'rbcs and p35S sense-3'rbcs	tobacco ( <i>Nicotiana tabaccum</i> L. cv. Petit Havana SR1)	<i>Nicotiana plumbaginifolia</i> L. and cotton ( <i>Gossypium hirsutum</i> L.)	fragments : cat1-1118bp; cat2-1070bp; ?	Charnongpol S et al. (1996) <i>Plant J</i> 10(3), 491-503; Wilkens H et al. (1997) <i>EMBO J</i> 16, 4806-4816; Charnongpol S et al. (1998) <i>Proc Natl Acad Sci USA</i> 95, 5818-5823; Mittler et al. (1995) <i>Proc Natl Acad Sci USA</i> 92(24), 14165-14170 --> see APXI
88	Cat1 and/or Cat2 (plant catalases)	H2O2 detoxification; role in pathogen defense		reduction in catalase activity and activation of plant defenses; high (>90%) catalase reduction; chlorosis or necrosis	p35S-antisense nos terminator	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	fragments but with full ORF	Takahashi H et al. (1997) <i>Plant J</i> 11(5), 993-1005
89	Catalase	H2O2 detoxification	?	constitutive expression of PR 1 genes	7-antisense-	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	?	Chen ZX et al. (1995) <i>Proc Natl Acad Sci USA</i> 92(10), 4134-4137
90	StCbl (cystathione beta-lyase; EC 4.4.1.8))	Methionine biosynthesis	vegetative tissue	reduction in Methionine levels bushy growth habit, small light green leaves and small tubers	p35S-antisense nos terminator	potato ( <i>Solanum tuberosum</i> )	potato ( <i>Solanum tuberosum</i> )	full-length cDNA clone (1.6kb)	Maimann et al (2000) <i>Plant J</i> 23, 747-758
91	CCA1	phytochrome signal transduction pathway	?	reduced phytochrome induction of the endogenous Lhcb1-3 gene	p35S-antisense (pBI121-Clontech)	<i>Arabidopsis thaliana</i> L. cv. Columbia	<i>Arabidopsis thaliana</i> L.	fragments ???	Wang ZY et al. (1997) <i>Plant Cell</i> 9(4), 491-507
92	CCoAOMT1 or 9(Caffeoyl-CoA O-methyltransferase) or CAOMT or CCoAOMT9 + CAOMT	lignin biosynthesis	in all lignifying cells	decrease in lignin content and alteration in lignin composition	p35S-antisense nos terminator	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	full-length of isolated cDNA (?)	Zhong R et al. (1998) <i>Plant Cell</i> 10(12), 2033-2046
93	CCoAOMT (Caffeoyl-CoA O-methyltransferase)	lignin biosynthesis	in all lignifying cells	significant decrease in total lignin content; wood coloration	p35S-antisense ; pBI121-Clontech	woody poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	woody poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	full-length of isolated cDNA (?)	Zhong R et al. (2000) <i>Plant Physiol</i> 124(2), 563-578
94	CCR (cinnamoyl-CoA reductase; EC 1.2.1.44)	lignin monomer biosynthetic pathway	?	altered lignin composition	p35S-antisense nos terminator or p35S+double enhancer-antisense-35S terminator	tobacco ( <i>Nicotiana tabaccum</i> L.)	tobacco ( <i>Nicotiana tabaccum</i> L.)	full-length(35 S-Tnos or 35SDE-T35S) or fragment( 35SDE-T35S)	Piquemal J et al. (1998) <i>Plant J</i> 13(1), 71-83; Ralph J et al. (1998) <i>Proc Natl Acad Sci USA</i> 95(22), 12803-12808

	A	B	C	D	E	F	G	H	I
95	CDPK (a protein kinase)	required for germination and pollen tube growth	(pollen specific - late stage of pollen development)	impaired <i>in-vitro</i> germination and pollen tube growth	antisense oligonucleotide s (24bp-DNA) (and sense?)	<i>Zea mays</i> L.	<i>Zea mays</i> L.	small 24bp fragments	Estruch JJ et al. (1994) Proc Natl Acad Sci USA 91(19), 8837-8841
96	Cel1 (endo-1,4-beta-glucanase)	flower abscission	increased mRNA abundance in abscission zone	partial reduction in flower abscission	p7-antisense-	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	???	Gonzalez-Bosch C et al. (1997) Plant Physiol 114(4), 1541-1546 = Lashbrook CC et al. Unpublished data
97	Cel2 (endo-1,4-beta-glucanase : cellulase)	contributes to cell wall disassembly in cell separation during fruit abscission	increased mRNA abundance during fruit ripening and in abscising flower abscission zones	delay in fruit abscision?	p35S-antisense nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill. cv. T5)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	truncated cDNA fragment (with full-length coding region)	Brummell DA et al. (1999) Plant Mol Biol (1999) 40(4), 615-622
98	cen-like protein 5	Repressor of flowering	young vegetative tissue	stunted growth, early flowering	anti-sense				Bradley et al unpublished ; Genbank gi:5453319
99	CGS (cystathione gamma-synthase)	role in methionine synthesis	?	severe growth retardation and morphological abnormalities, from germination to flowering	antisense	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>		Gakiere B et al. (2000) C R Acad Sci III 323(10), 841-851
100	chs A	Pigment biosynthesis	flowers, leaves of stressed plants	inhibition of flower pigmentation	p35S-antisense nos terminator	petunia ( <i>Petunia hybrida</i> L.) and tobacco ( <i>Nicotiana tabacum</i> L. cv. SR1)	petunia ( <i>Petunia hybrida</i> L. cv. VR)	3'half of chs	van der Krol et al (1988) Nature 333, 866-869 ; van der Krol et al (1990) Mol. Gen. Genet. 220, 204-212; van der Krol et al (1990) Plant Mol Biol 14(4), 457-466
101	chs	Pigment biosynthesis	flowers	reduced floral pigmentation	p35S-sense-, p35S-antisense-, p-less sense	petunia ( <i>Petunia hybrida</i> L.)	petunia ( <i>Petunia hybrida</i> L.)	different genomic constructs	van der Krol et al (1990) Plant Cell 2, 291-299
102	chs	Chalcon synthase (anthocyanin and flavonoid synthesis)	flowers	loss of flower pigmentation	p35S-sense, p35S-a.s.	petunia			Napoli et al (1990) Plant Cell 2, 279-289; Jorgensen et al (1996) PMB 31(5), 957-973; Que et al. (1997) Plant Cell 9, 1357-1368 ; Que et al (1998) Plant Journal 13, 401-409; Stam M et al. (2000) Plant Journal 21(1), 27-42
103	chs	Pigment biosynthesis and gametophyte development	anthers	loss of anther pigmentation and male sterility	anther specific promoter - antisense	petunia			van der Meer et al. (1992) Plant Cell 4(3) 253-262
104	chs	pigment biosynthesis	flowers, leaves of stressed plants	reduced mRNA; silencing impaired by <i>hog1</i> and <i>ddm1</i> mutations!	pCHS-sense-tCHS	<i>Arabidopsis thaliana</i> L. Landsberg erecta	<i>Arabidopsis thaliana</i> L. cv. Columbia	3.9 kb of genomic sequence with entire CHS gene	Davies et al (1997) Plant Journal 12, 791-804; Fumer et al (1998) Genetics 149, 651-652
105	chs	pigment biosynthesis	flower petals, 3-fold lower expression in leaf tissue...	reduced mRNA, white or pale-pink flowers, stability is discussed	p35S/Cab L-sense or antisense-trios (pAGS802 binary vector)	<i>Chrysanthemum</i> cultivar Moneymaker	<i>Chrysanthemum</i> cultivar Debonair	cDNA (+/-1kb)	Courtney-Gutierrez et al. (1994) Biotechnology 12(3), 268-271
106	chs IV	pigment biosynthesis	stems	flavonoid-deficiency, reduced chs expression; (enhanced adventitious root formation?)	p35S(duplicated)-antisense-3'-rbcS	walnut ( <i>Juglans nigra</i> * <i>Juglans regia</i> )	walnut	400bp of cDNA	Eli Euch C et al. (1998) Plant Mol Biol 38(3), 467-479
107	chs 17	tannin biosynthesis	?	increased tannin accumulation and increased endogenous CHS mRNA	p35S-antisense nos terminator	<i>Lotus corniculatus</i> L.	<i>Phaseolus vulgaris</i> (CHS17)	full length cDNA	Coliver SP et al. (1997) Plant Mol Biol 35(4), 509-522
108	class I chitinase	chitin hydrolysis of fungal cell walls	upon fungal infection	slightly faster rate of disease (not significant!) + reduced chitinase levels	p35S-antisense nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length cDNA (0.9kb)	Samac DA and Shah DM (1994) Plant Mol Biol 25(4), 587-596
109	CHL H (Mg-chelatase subunit H)	intermediate in the chlorophyll synthesis: tetrapyrrole biosynthesis pathway	young leaves (chloroplasts)	reduced growth rate and chlorophyll deficiency	p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L. cv Samsun NN)	tobacco ( <i>Nicotiana tabacum</i> L.)	partial cDNA fragment (3.5kb/4.5 kb)	Papenbrock et al. (2000) Plant Physiol 122(4), 1161-1169
110	CHL I (Mg-chelatase subunit I)	intermediate in the chlorophyll synthesis: tetrapyrrole biosynthesis pathway	young leaves (chloroplasts)	reduced green pigmentation	p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length cDNA (1.4kb)	Papenbrock et al. (2000) Plant J 22(2), 155-164
111	CIP7	positive regulator of light-regulated genes	elevated expression in light grown seedlings (COP1 and light regulated)	defects in light dependant anthocyanin and chlorophyll accumulation	p35S-antisense nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	C-terminal half of CIP7 cDNA	Yamamoto YY et al. (1998) Plant Cell 10(7), 1083-1094
112	AthCK2A1 (CK2: caseine kinase II):	involved in DNA replication and transcription, RNA processing and translation, cell metabolism, and motility of cells	ubiquitous and is essential for survival	smaller adult leaf size and increased expression of chs in darkness...	p35S-antisense CK2-alpha subunit-rbcS	<i>Arabidopsis thaliana</i> L. cv. Wassilewskija	<i>Arabidopsis thaliana</i> L.	coding region (928bp)	Lee Y et al. (1999) Plant Physiol 119(3), 989-1000
113	agamous (ag) and clavata 3 and apetala 1 and perianthia	floral identity genes	flowers	flower aberration	dsRNAi = p35S-sense + GUS-loop + antisense-	arabidopsis ( <i>Arabidopsis thaliana</i> L.)	arabidopsis ( <i>Arabidopsis thaliana</i> L.)	fragments	Chuang and Meyerowitz (2000) Proc. Natl. Acad. Sci. 97(9), 4985-4990
114	COMT (caffeic acid O-methyl transferase)	lignin biosynthesis	xylem(?)	larger xylem cells: decreased enzyme activity; reduction in lignin content(42 to 85%)	p35S/tobacco etch virus UTR-antisense- (35S	tobacco ( <i>Nicotiana tabacum</i> L. cv. Xanthi)	alfalfa ( <i>Medicago sativa</i> L.); lucem?	cDNA fragment (430bp)	Ni W et al. (1994) Transgenic Res 3, 120-126
115	COMT (caffeic acid O-methyl transferase)	lignin biosynthesis	woody tissues	substantial reduction (17%) of lignin levels in 6-months-old trees	p35S(double) - sense-35S ter (co-suppression)	poplar ( <i>Populus tremula</i> * <i>Populus trichocarpa</i> )	poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	1.3kb cDNA (full length coding sequence)	Jouanin L et al. (2000) Plant Physiol 123(4), 1363-1374
116	COMT or CAD or COMT+CAD (double antisense transformation)	lignin biosynthesis	woody tissues	red coloration mainly in the outer xylem; changed lignin compositions	p35S-antisense or sense-T7; p7- CAD sense-?	poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	poplar ( <i>Populus tremula</i> * <i>Populus alba</i> )	cDNA-fragments : 0.6kb and 0.9kb and 1.5kb (sense)	Van Doornelaere J et al. (1995) 8(8), 855-864; Lapierre C et al. (1999) Plant Physiol 119(1), 153-164

	A	B	C	D	E	F	G	H	I
117	CP29 or CP28 (chlorophyl a/b binding proteins)	role in light harvesting and energy dissipation within the photosynthetic apparatus	green tissues	remarkably low amounts of target proteins; removal affected the photosystem II function; overall photosynthetic rates remained similar to wt	p35S-antisense ?	arabidopsis ( <i>Arabidopsis thaliana</i> L. cv. Columbia)	arabidopsis ( <i>Arabidopsis thaliana</i> L.)	cDNA-fragments : 7kb for CP29 and 7kb for CP28	Andersson J et al. (2001) The Plant Cell 13(), 1193-1204
118	CPO (coproporphyrinogen oxidase; X92831)	plastid/nucleus signalling?	CPO is exclusively located in stroma of plastids	reduced gene activity: growth retardation and necrosis (oxidative leaf damage)	p35S-antisense ocs terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	a 1191 bp sequence (full-length)	Kruse E et al. (1995) EMBO J 14(15), 3712-3720; Mock H-P et al. (1999) J Biol Chem 274(7), 4231-4238 (see UROD)
119	mCS (mitochondrial cyrate synthase)	first enzyme in the tricarboxylic acid (TCA) cycle	all tissues	reduction (6% to <30% from WT) of citrate synthase activity; specific disintegration of the ovary tissue of flowers (= flower abortion)	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> )	potato ( <i>Solanum tuberosum</i> )	1.9kb cDNA	Landschutze V et al. (1995) EMBO Journal 14(4), 660-666
120	cys1 (O-acetylyserine (thiol) lyase) - EC4.2.9.8	cysteine biosynthesis	roots and green tissue (wheat), leaves (other plants)	no effect in tobacco plants	p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	wheat ( <i>Triticum aestivum</i> L. cv April Bearded)	1.27kb cDNA fragment	Youssefian S et al. (1993) Plant J 4(5), 759-769
121	DAHP synthase (3 deoxy-D-arabino-heptulonate-7-phosphate synthase); shkA gene	first enzyme in the shikimate pathway	wound inducible	reduced stem length, stem diameter, and reduced stem lignification; (no co-suppression detected...)	p35S-antisense rbcS	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	genomic part of the gene (exon + intron parts): 800bp	Jones JD et al. (1995) Plant Physiol 108, 1413-1421
122	D-enzyme (4-alpha glucanotransferase, disproporportionating enzyme, EC 2.4.1.25)	role in potato starch metabolism; production of cycloamylose	leaves, stems, roots and stolons; increase of mRNA in leaves upon light 'treatment'	reduction of activity for sense and antisense transgenes; slow plant growth	ppalatin-antisense or sense-nos terminator; p35S-sense or antisense-nos terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	2.1kb cDNA fragment	Takahashi T et al. (1998) Planta 205(3), 445-451
123	delta 12 or delta 15 desaturases	role in saturation of C18 fatty acids	??	modified fatty acid contents in seeds	pAT2S2 (seed specific)-antisense-; pAT2S2-sense-	arabidopsis ( <i>Arabidopsis thaliana</i> L.)	delta12; <i>Arabidopsis thaliana</i> L.; delta 15; rapeseed		Cartea ME et al. (1998) Plant Science 136(2), 181-192
124	omega-3 fatty acid desaturase (FAD7)	synthesis of trienoic fatty acids	in chloroplasts	lower trienoic fatty acid contents; better acclimation to higher temperatures	p35S-sense	tobacco ( <i>Nicotiana tabacum</i> L.)			Kodama et al (submitted EMBO 1997); Murakami Y. et al. (2000) Science 287(5452), 476-479 (see FAD7...)
125	omega-3 fatty acid desaturase (plastidial)	synthesis of trienoic fatty acids	upon wounding	marked reduction of transcript; up to 60% reduction of trienoic acids; reduction of reaction upon wounding	p??-antisense-	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)		Martin M et al. (1999) Eur J Biochem 262(2), 283-290
126	DFR (A1 gene)	Pigment biosynthesis	flowers	reduced floral pigmentation	p35S-sense-35S terminator	petunia ( <i>Petunia hybrida</i> L.)	maize ( <i>Zea mays</i> )	full-length cDNA 1320bp type 2 A1 gene	Mayer P et al. (1987) Nature 330, 677-678
127	DFR (see CHS)	Pigment biosynthesis	flowers	reduced floral pigmentation	p35S-sense-nos terminator	petunia	petunia	cDNA fragment of 1.3kb	van der Krol et al (1990) Plant Cell 2, 291-299
128	DFR	condensed tannins condensation	overall	reduction of tannins in leaf, stem and root tissue (not very clear)	p7-sense-; p35S-antisense-nos terminator	<i>Lotus corniculatus</i> L.	<i>Antirrhinum majus</i> L.	full-length cDNA (1.4kb); 3 different cDNA fragments : 0.5-1-0.9kb	Caron TR et al. (1994) Theor Appl Genet 87, 1006-1015; Bavage AD et al. (1997) Plant Mol Biol 35(4), 443-458; Robbins et al. (1998) Plant Physiol 118(3), 1133-1144
129	Dof1	transcription factors unique to plants	?	reduction of specific genes targeted by dof1	p35SC4PPDK-antisense-nos terminator	Maize leaf-protoplasts	maize ( <i>Zea mays</i> )	cDNA fragment (7kb)	Yanagisawa S (2000) Plant J 21(3), 281-288
130	DOH1 (homeobox gene)	key role in maintaining the basic plant architecture	meristem-rich tissues	multiple shoot apical meristem formation and early flowering	p35S-antisense	orchid ( <i>Dendrobium Madame Thong-in</i> )	orchid ( <i>Dendrobium Madame Thong-in</i> )	entire cDNA (1.4kb)	Yu H et al. (2000) Plant Cell 12(11), 2143-2160
131	E6	Function is not yet known...	fiber specific	reduced E6 protein levels (60 to 98%)	pE6-antisense-nos terminator; p35S-antisense	cotton sp. ( <i>Gossypium hirsutum</i> L. and <i>G. barbadense</i> L.)	cotton sp. ( <i>Gossypium hirsutum</i> L.)	entire (?) cDNA (+/- 0.8kb)	John ME (1996) Plant Mol Biol 30(2), 297-306
132	E8 (a dioxygenase; X13437)	negative effect on ethylene production (enzyme related to ACC oxydase)	fruit specific; transcriptionally activated at the onset of ripening	reduced E8 protein level during fruit ripening and increase in ethylene evolution specifically during ripening of detached fruit	p35S-antisense	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	full-length cDNA (3kb)	Peláez Rubia L et al. (1992) Plant Cell 4(6), 681-687
133	EG (endo-beta-1,4-glucanase; cel1')	specific cleavage of beta-1,4-glucosyl linkages of xyloglucan	late stage in ripening fruit	strong down regulation of cel1 transcripts with a higher proportion of sense transfectants that showed down regulation; no statistical difference in fruit firmness and EG activity between transfectants and wild type plants	p35S-antisense or sense-trios	strawberry ( <i>Fragaria x ananassa</i> Duch. cv. Brighton)	strawberry ( <i>Fragaria x ananassa</i> Duch. cv. Calypso)	full-length cDNA (1.779kb)	Lindsey C et al. (2001) Planta 214, 11-21
134	BnF5H1-3 (putative ferulate-5-hydrolyase)	Sinapine biosynthesis	maximal expression in stems and minimal in seeds	sinapine reduction (to 40%) in seeds; no detectable effect on the transcription levels	p35S - antisense-nos terminator; pnipin-antisense-nos terminator; pnipin-sense-nos terminator	Brassica napus	Brassica napus	cDNA fragment of 1.8kb lacking poly A region	Nair RB et al. (2000) Plant Physiol 123(4), 1623-1634

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135	NtFAD3 (omega-3 fatty acid desaturase; D26509)	biosynthesis of linolenic acid (18:3)	enzyme located in microsomes and plastid membranes	up to 30% reduction in NtFad3 mRNA; decrease of up to 80% in 18:3 lipids	p35S-antisense nos (pBI121 binary vector)	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment of 0.5kb : 3' flanking region + part of coding region	Hamada T et al. (1998) Transgenic Res. 5(2), 115-121
136	AtFATB1 (acyl-acyl carrier protein thioesterase B1)	contribution to palmitate (16:0) production	flowers and seeds	reduced content of palmitate in flowers and seeds	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA coding region (2kb)	Dörmann P et al. (2000) Plant Physiol 123(2), 637-644
137	fbp1 (MADS-box gene) - floral binding protein 1	control of floral development	only expressed in petals and stamen (class B)	flower aberration	p35S/ADH intron-sense nos (pBIN19 vector)	petunia ( <i>Petunia hybrida</i> - W115 variety)	petunia ( <i>Petunia hybrida</i> )	full-length fbp1 cDNA (780bp)	Angenent et al. (1993) Plant Journal 4(1), 101-112
138	cFBPase (cytosolic fructose-1,6-biphosphatase) or SPS (sucrose phosphate synthase)	photosynthetic carbon metabolism	leaves	inhibition of sucrose synthesis and starch accumulation for AS cFBPase and no starch accumulation for AS SPS	p35S-antisense nos	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cFBPase: full length: 1060bp; SPS: 1810bp- partial clone	Strand et al. (2000) Plant J 23(6), 759-770
139	FBPase (cytosolic)	regulation on the rate of sucrose synthesis		limitation in sucrose biosynthesis	p35S-antisense nos	potato ( <i>Solanum tuberosum</i> cv Désirée)	potato ( <i>Solanum tuberosum</i> cv Désirée)	1487bp cDNA	Zrenner et al. (1996) Plant Journal 9(5), 671-681
140	SiGA20ox1	Synthesis of gibberellins (GA): role in the control of stem elongation and tuber induction	leaves (regulated by daylight)	shorter stems, decreased length of the internodes and earlier tuberization (6/35 primary transformants)	p35S-antisense nos	potato ( <i>Solanum tuberosum</i> ssp. andigena)	potato ( <i>Solanum tuberosum</i> )	420bp 5' cDNA region	Carrera E et al. (2000) Plant J 22(3), 247-256
141	AtGA20ox1,2 and 3	GA-biosynthesis	differential expression of the 3 genes	GA20ox1: short hypocotyls and reduced rates of stem elongation; GA20ox2: influence on stem growth (1 transformant); GA20ox3: short hypocotyls (1 transformant)	p35S(double)-antisense-tml end(?)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNAs: ox1: 1.3bp ox2: 1.4bp ox3: 1.4bp	Coles JP et al. (1999) Plant J 17(5), 547-558
142	GAPDH (chloroplast loc GAPDH - A subunit)	reduction of PGA to triose phosphate - key step to photosynthesis	thylacoids	reduced GAPDH activity (11 to 24% of WT)	p7-antisense-	tobacco			Price GD et al. (1995) Planta 195(3), 369-378
143	GBSS (Waxy protein from Cassava)	granule-bound starch synthase (low copy nr.) = starch synthesis	tuber	complete inhibition of endogenous gene = absence of GBSS protein + amylose (amylose-free potato)	pGBSS-5'antisense+3'sense-nos	potato ( <i>Solanum tuberosum</i> L.)	cassava ( <i>Manihot esculenta</i> Crantz.)	full-length cDNA (5':1.5kb; 3':0.6kb)	Salehuzzaman et al. (1993) Plant Mol Biol 23(5), 947-962
144	GBSS (granule-bound starch synthase; EC 24.1.2.1)	starch biosynthesis	tuber	tubers containing amylose-free starch	P35S-antisense nos; PGBSS-antisense-	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (2.3kb)	Visser RGF et al. (1991) Mol Gen Genet 225, 289-296; Kuipers AGJ et al. (1994) Plant Mol Biol 26(6), 1759-1773; Kuipers AGJ et al. (1995) Mol Gen Genet 246(6), 745-755; Kull B et al. (1995) J Genet Breed 49, 69-76; Wolters et al. (1998) Mol Breed 4, 343-358
145	GBSS	starch biosynthesis	tuber	tubers containing amylose-free starch	P35S-antisense nos; PGBSS-antisense-; p35S-sense-nos	potato	potato, cassava	full length cDNA and genomic sequence s	Kuipers AGJ et al. (1992) Euphytica 59, 83-91; Kuipers AGJ et al. (1994) Plant Mol Biol 26(6), 1759-1773; Kuipers AGJ et al. (1995) Mol Gen Genet 246(6), 745-755; Kull B et al. (1995) J Genet Breed 49, 69-76; Wolters et al. (1998) Mol Breed 4, 343-358
146	GBSSI	starch biosynthesis: catalysis of the production of amylose	tuber	production of amylose free starch	p35S-sense-; pGBSS-sense-; p7-antisense-	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	cDNA and genomic sequence s	Filipe E et al. (1996) Plant Mol Biol 31, 731-739; Wolters and Visser (2000) Plant Mol Biol 43(2-3), 377-386
147	GER1 (bifunctional 3,5-epimerase-4-reductase)	role in L-fructose synthesis	predominant expression in roots and flowers	very significant reduction of enzyme activity;	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full length cDNA(?)	Bonin CP and Reiter WD (2000) Plant Journal 21(5), 445-454
148	GF14-epsilon and $\mu$ (a 14-3-3 protein)	regulation of the starch accumulation	leaves (chloroplast-starch granules)	dramatic increase in starch accumulation in leaves	p7-antisense- (pBI121 vector from clontech)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA (???)	Sehnke PC et al. (2001) Proc Natl Acad Sci USA 98(2), 765-770
149	gigantea (GI)	phytochrome B signalling, flowering time	vegetative tissue	late flowering	SKO	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	genomic sequence (3.6kb)	Huq et al (2000) Proc Natl Acad Sci USA 97, 9789-9794
150	GLA (An isoform of tobacco class-I beta-1,3-glucanase)	has an important role in pathogenesis	upon pathogen en ethylene induction (?)	reduced lesion size and number in virus-infected local-lesion hosts	p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.) and <i>Nicotiana sylvestris</i>	tobacco ( <i>Nicotiana tabacum</i> L.)	coding region (581bp)	Neuhaus JM et al. (1992) Plant Mol Biol 19(5), 803-813; Beffa R and Meins F Jr (1996) Gene 179(1), 97-103; Beffa RS et al. (1993) PNAS USA 90, 8792-8796
151	GMPase (GDP-mannose pyrophosphatase)	biosynthesis of cell-wall-biosynthesis precursors; synthesis of ascorbate	ubiquitous with the highest expression in stems, sink leaves and small tubers	when transferred into soil: dark spots on leaf veins and stems till total senescence after 3 months in soil	p35S-antisense nos	potato ( <i>Solanum tuberosum</i> )	potato ( <i>Solanum tuberosum</i> )	cDNA clone (1.5kb)	Keller R et al. (1999) Plant J 19(2), 131-141
152	GN1 (beta-1,3-glucanase) or CHN	has an important role in pathogenesis; glucan degradation	roots and flowers (without stress) and, pathogen or stress induced	reduced mRNA	p35S-sense-	<i>Nicotiana sylvestris</i>	<i>Nicotiana tabacum</i>	GN1: coding region (581bp); CHN: ???	Holtorf H et al. (1999) Plant Cell 11(3), 471-481; Kunz C et al. (2001) Planta 212, 243-249
153	GN1 (beta-1,3-glucanase)	has an important role in pathogenesis; glucan degradation	stress induced	suppressed mRNA	p35S-sense-tgn1(1.35kb)	<i>Nicotiana tabacum</i> L. cv SR1	<i>Nicotiana plumbaginifolia</i>	DNA fragment (3.3kb)	de Carvalho F et al. (1992) EMBO J 11, 2595-2602; de Carvalho Nielbel F et al. (1995) Plant Cell 7, 347-358
154	GnTI (N-acetyl glucosaminyltransferase I)	role in complex glycan formation	constitutive	reduction in amount of protein	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> ) and tobacco ( <i>Nicotiana tabacum</i> )	potato ( <i>Solanum tuberosum</i> ) and tobacco ( <i>Nicotiana tabacum</i> )	complete cDNA clones tobacco: 1.72kb; potato: 1.66kb	Wenderoth I and Schaewen A (2000) Plant Physiol 123(3), 1097-1108
155	GO (glycolate oxidase)	an enzyme in the glycolate pathway	green tissues	photo-bleaching of leaf colour and drastic growth inhibition	P35S-sense-	tobacco ( <i>Nicotiana tabacum</i> L. cv SR1)	pumpkin	full-length cDNA (7kb)	Yamaguchi K and Nishimura M (2000) Plant Cell Physiol 41(12), 1397-1406

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156	GRCD1 (AGL2-like MADS box gene; AJ400623)	role in determining the stamen identity	developing stamen and carpel; flower-specific	flower aberration	P35S-antisense	<i>Gerbera hybrida</i>	<i>Gerbera hybrida</i>	near full-length cDNA (20 bp missing in 5': 874bp)	Kotilainen M et al. (2000) Plant Cell 12(10), 1893-1902
157	GS1 (glutamine synthetase; EC 6.3.1.2)	catalysis of the ATP-dependent condensation of NH3 with glutamate to produce glutamine	cytoplasmic; over with differential expression	No decrease in mRNA; significant decrease in the level of both GS1 and GS2 and GS activity	P35S-antisense-nos (pMON316)	tobacco ( <i>Nicotiana tabacum</i> L.)	alfalfa ( <i>Medicago sativa</i> )	cDNA fragment (1.35kb)	Temple SJ et al. (1993) Mol Gen Genet 236(2-3), 315-325
158	GS1 (glutamine synthetase)	catalysis of the ATP-dependent condensation of NH3 with glutamate to produce glutamine	cytoplasmic; over with differential expression	80% decrease in transcript level but no reduction of GS activity or GS1 polypeptide level	P35S- HTsense+anti sense(3'fragme nts)-nos terminator	alfalfa ( <i>Medicago sativa</i> )	alfalfa ( <i>Medicago sativa</i> )	cDNA fragment (209bp 3'UTR); fusion protein!	Temple SJ et al. (1998) Plant Mol Biol 37(3), 535-547
159	AthH2	putative channel protein of the plasmalemma	temporally activated by light in expanding and/or differentiating cells	reduction in water uptake of protoplasts	P35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	???	Kaldenhoff R et al. (1995) Plant J 7(1), 87-95
160	HAESA (receptor-like protein kinase; RLK5; MB4660)	control of floral organ abscission	expression in the abscission zones	delayed abscission of floral organs correlated with HAESA-protein amount	P35S-antisense (pGA482)	<i>Arabidopsis thaliana</i> L. ec. Colombia	<i>Arabidopsis thaliana</i> L.	full-length cDNA (+3185bp)	Jinn TL et al. (2000) Genes Dev 14(1), 108-117
161	tonoplast H <sup>+</sup> -ATPase	proton translocation machinery: ion and metabolite transport	depending on the isophorms	altered leaf morphology and reduced cell expansion	p35S-antisense 7' terminator	carrot ( <i>Daucus carota</i> L.)	carrot ( <i>Daucus carota</i> L.)	full-length cDNA (+1kb) and 5'untransl. region (150bp)	Gogarten et al (1992) Plant Cell 4(7), 851-864; Perez C and Boulter M (1994) Symp Soc Exp Biol 48, 11-22; Xie J et al. (1996) J Cell Sci 109(Pt2), 489-497; Morosomme P and Boulter M (2000) Biochim Biophys Acta 1465(1-2), 1-16
162	H1B (variant B of the major somatic histone)	chromosome packaging; role in male meiosis and subsequent development of pollen grains	ubiquitous	characteristic aberrations in flower development and almost completely male sterile; decrease in chromosome packaging	p35S(E)- antisense-35S	tobacco ( <i>Nicotiana tabacum</i> L. cv. SR1)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length cDNA (1104bp)	Prymakowska-Bosak M et al. (1999) Plant Cell 11(12), 2317-2329
163	HB (hemoglobin)	nonsymbiotic hemoglobins: oxygen sequestration under stress conditions	?	no RNA data; downregulation of protein levels; change in energy status under hypoxia	pUB11- antisense-?	maize (var. BMS) cells	barley	cDNA (ORF: 7bp)	Sowa AW et al. (1998) Proc Natl Acad Sci USA 95(17), 10317-10321
164	AtHD1 (histone deacetylase)	control of gene expression during development: a global regulator (transcriptional gene silencing)		various developmental abnormalities; dramatic reduction (till 40%) in endogenous transcript: accumulation of acetylated histones (H4)	p35S-antisense	<i>Arabidopsis thaliana</i> L. (Columbia)	<i>Arabidopsis thaliana</i> L. (Columbia)	full-length cDNA (1.5kb)	Tian L and Chen ZJ et al. (2001) Proc Natl Acad Sci USA 98(1), 200-205
165	AtHD2A (histone deacetylase)	important in the reproductive development: repression of transcription	flowers and young siliques	seed abortion	p-394CUP- antisense-	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L. (Columbia)	full-length cDNA (736bp)	Wu K et al. (2000) Plant J 22(1), 19-27
166	HIC (for high carbon dioxide)	encodes a negative regulator of stomatal development that responds to CO <sub>2</sub> concentration	guard cell specific	significant increase in stomatal density in response to an increase in CO <sub>2</sub> ; decrease in HIC mRNA, mostly undetectable	p35S-antisense ocs terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> (C24 ecotype)	full-length cDNA (2073bp)	Gray JE et al (2000) Nature 408, 713-716
167	hmg1 (3-hydroxy-3methylglutaryl-CoA reductase)	key enzyme involved in the metabolism of terpenoid compounds	??	Delayed development and changes in flower colours and shape	p35S(2x)-sense or antisense-?	tobacco ( <i>Nicotiana tabacum</i> L.)	<i>Arabidopsis thaliana</i> L.	?	Parolko VA et al. (2000) Genetika 36(9), 1200-1205
168	HPR (hydroperpyruvate reductase, EC 1.1.1.29)	integral part of the glycolate pathway: photorespiration	leaves...	reduction of HPR-activity but no clear mRNA reduction of endogenous gene	p35S-antisense nos (pMON316 vector)	tobacco ( <i>Nicotiana tabacum</i> L.)	cucumber ( <i>Cucumis sativus</i> cv. Improved Long Green)	full-length cDNA (1.5kb)	Oliver MJ et al. (1993) Mol Gen Genet 239(3), 425-434
169	HSP101 (Heat shock protein)	plays a pivotal role in heat shock tolerance	after heat induction and in germinating seeds	diminished capacity to acquire heat tolerance after mild conditioning pretreatments	p35S-sense or antisense	<i>Arabidopsis thaliana</i> L. (Columbia or Nössner)	<i>Arabidopsis thaliana</i> L. (Columbia)	full-length cDNA (3124bp)	Queitsch C et al. (2000) Plant Cell 12(4), 479-492
170	StHK1 (Hexokinase 1; X94302)	transport of sugars	leaves and developing tubers	starch accumulation at the end of the night period	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	EST- fragment (1.3kb/1.7 kb)	Varamendi et al. (1999) Plant Physiol 121(1), 123-134
171	hydroperoxide lyase	route of hydroperoxide degradation	leaves?	reduced activity; increase (38%) of Lipid hydroperoxidase (LHPO) in leaves	antisense	potato			Griffiths G et al. (2000) J Exp Bot 51(349), 1363-1370
172	acid-Invertases (cell wall and vacuolar invertases)	important function in sucrose partitioning	overall	important phenotypic alterations; sucrose and starch accumulation	p35S-antisense	carrot ( <i>Daucus carota</i> L.)	carrot ( <i>Daucus carota</i> L. cv. Nantaise)	full-length cDNA (cw:1816bp; vac:2024bp)	Tang GQ et al. (1999) Plant Cell 11(2), 177-189
173	cold-inducible soluble acid Invertase	involved in the regulation of the tuber hexose to sucrose ratio	upon cold induction	decreased hexose and increased sucrose content in tubers	p35S-antisense	potato ( <i>Solanum tuberosum</i> L.)			Zrenner R et al. (1996) Planta 198(2), 248-252
174	Intracellular soluble acid Invertase - TIV1 (beta-fructosidase; EC 3.2.1.26)	involved in the regulation of the fruit hexose to sucrose ratio	fruit	decreased hexose and increased sucrose content in fruits; smaller ripe fruits	p35S-antisense	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	5'cDNA- fragment (1640bp-75% coding reg.)	Kiann EM et al. (1996) Plant Physiol 112(3), 1321-1330
175	LAT52 (X15855)	a glycosidated heat-stable protein (yet unknown function)	pollen	abnormal hydration and germination of the pollen: no fertilization possible	LAT52 promoter antisense-nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	full-length cDNA (1810bp)	McCormick S et al. (1991) Trends Genet 7, 298-303; Muschietti J et al. (1994) Plant J 6(3), 321-338

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176	Lhca2 and Lhca3 (light harvesting proteins)	role in Photosynthesis	green tissues	downregulation of Lhca2 in antisense Lhca3 and the reverse is also true	p35S-antisense	<i>Arabidopsis thaliana</i> L. ecotype Columbia	<i>Arabidopsis thaliana</i> L.	cDNA-fragment (7bp)	Ganeteg U et al. (2001) <i>Plant Physiol.</i> 127(), 150-158
177	Lhca4	photosystem 1 type IV chlorophyll a/b-binding protein; role in photosynthesis	green tissues	alteration in the low-temperature fluorescence emission spectrum; unexplainable delay in flowering and an increase in seed weight	p35S-antisense-nos terminator	<i>Arabidopsis thaliana</i> L. ecotype C24	<i>Arabidopsis thaliana</i> L.	cDNA-fragment (1006bp)	Zhang H et al. (1997) <i>Plant Physiol.</i> 115(4), 1525-1531
178	Lhcb1-2	chlorophyll a/b-binding protein of light-harvesting complex II (LHCII); role in photosynthesis	green tissues	no influence on the phenotype; significant reduction of transcript	pE35S-antisense-35S-terminator; pPTE-antisense-35S terminator	tobacco ( <i>Nicotiana tabacum</i> L. cv Petit Havanna SR1)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA-fragment (509bp; 105bp: transit sequence)	Flachmann R and Kühlbrandt W (1995) <i>Plant Cell</i> 7(2), 149-160; Flachmann R (1997) <i>Plant Physiol.</i> 113(3), 787-794
179	NtLIM1 (Pal-box binding protein)	Important cis acting element for gene expression involved in lignin biosynthesis	stem, but also present in leaves and roots	27% reduction of lignin content; low level of transcripts from some key phenylpropanoid pathway genes	p35S-antisense-nos terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	1.0kb fragment	Kawaoka A et al. (2000) <i>Plant J.</i> 22(4), 289-301
180	Lol p 5	major allergenic protein of Ryegrass	pollen	no detection possible of allergen by immunoblot analysis	pOry s1 (pollen-specific promoter) - antisense-	Ryegrass ( <i>Lolium rigidum</i> L.)	Ryegrass ( <i>Lolium rigidum</i> L.)	0.94kb cDNA fragment	Bhalla PL et al. (1999) <i>Proc Natl Acad Sci USA</i> 96(20), 11676-11680
181	LOX1= POTLX-1 (lipoxygenase; U60200)	plant associated lipoxygenase; role in the regulation of tuber enlargement	transcription restricted to developing tubers, stolons and roots	reduced tuber yield, decrease of average tuber size and disruption of tuber formation; transcription-reduction of other LOX genes...	p35S-antisense ??? (pCB201 binary vector)	potato ( <i>Solanum tuberosum</i> L. cv FL1607)	potato ( <i>Solanum tuberosum</i> L.)	cDNA-fragment (1076bp; coding sequence)	Kolomietz MV et al. (2001) <i>Plant Cell</i> 13(3), 613-626
182	LOX (lipoxygenase; X84040)	involvement in the establishment of incompatibility in plant-microorganism interactions	expression associated with certain developmental events and pathogen induced	reduced elicitor) and pathogen-induced LOX activity; compatible phenotype	p35S-antisense-nos terminator	<i>Nicotiana tabacum</i> L.	<i>Nicotiana tabacum</i> L.	full-length cDNA (2.9kb) or internal cDNA fragment (624bp)	Rance I et al. (1998) <i>Proc Natl Acad Sci USA</i> 95(11), 6554-6559
183	LOX (lipoxygenase)	responsible for hydroperoxide biosynthesis	senescent potato leaves?	reduced activity	p7-antisense-	potato			Griffiths G et al. (2000) <i>J Exp Bot</i> 51(349), 1363-1370
184	LOX-H3 (lipoxygenase)	plays a role in the regulation of wound-induced gene expression	wound-inducible	reduction of mRNA; abolished accumulation of proteinase inhibitors upon wounding; poorer performance toward insect herbivory and higher tuber yields	p35S-antisense-ocs terminator	potato ( <i>Solanum tuberosum</i> L. cv Désirée)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (3002bp)	Royo et al. (1999) <i>Proc Natl Acad Sci USA</i> 96(3), 1146-1151
185	OsLRK1 (leucine-rich repeat receptor like protein kinase)	putative role in floral meristem activity	in immature panicles	increased number of flower organs	p7-antisense-	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)		Kim CK et al. (2000) <i>Plant Science</i> 152(1), 17-26
186	OsMADS4 (Pistillata like) and OsMADS3 (Agamous like)	floral identity gene	flowers	floral aberration	maize ubiquitin promoter (Ubi1)-antisense-nos terminator	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)	cDNA-clones (7bp)	Kang HG et al. (1998) <i>Plant Mol Biol</i> 38(6), 1021-1029
187	MAL1 (beta glucosidase II)	glucosidase II activity: glycoprotein processing	tubers (microsomes)	extremely stunted phenotype, curled leaves, decrease in tuber yield... ER-stress.	p35S(2x)-antisense-	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	open reading frame-cDNA (2757bp)	Taylor et al. (2000) <i>Plant J.</i> 24(3), 305-316
188	MAL2 (beta glucosidase II)	glucosidase activity...?	tubers ?	reduction of transcript but no visible phenotype	p35S(2x)-antisense-(pBIN19)	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	open reading frame-cDNA (7bp)	Taylor et al. (2001) <i>Planta</i> 213(2), 258-264
189	MET1 (methyl transferase)	role in regulating many developmental pathways (dysregulation of gene expression?)	?	phenotypic and developmental abnormalities	p35S-antisense-nos terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (2.8kb; 4.3kb)	Finnegan et al. (1996) <i>Proc Natl Acad Sci</i> 93(16), 8449-8454; Ronenius MJ et al. (1996) <i>Science</i> 273, 654-657; Jacobsen and Meyerowitz (1997) <i>Science</i> 277(5329), 1100-1103; Genger RK et al. (1999) <i>Plant Mol Biol</i> 41, 269-278; Jacobsen et al. (2000) <i>Curr Biol</i> 10(4), 179-186
190	NtMET1 (DNA methyl transferase)	possible role in plant morphogenesis?	dividing cells	decrease in DNA-methylation; small leaves, short internodes, abnormal flower morphology	p35S-antisense-nos terminator (pBI121 vector)	tobacco ( <i>Nicotiana tabacum</i> L. cv. Bright Yellow)	tobacco ( <i>Nicotiana tabacum</i> L. cv. Bright Yellow)	cDNA fragment (1890bp)	Nakano Y et al. (2000) <i>Plant Cell Physiol</i> 41(4), 448-457
191	MOM	gene product is required for the maintenance of transcriptional gene silencing	?	transcript depletion: reactivation of transcription from several previously silent, heavily methylated loci with no changes on the methylation pattern	p35S-antisense-35S-terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	3' cDNA fragment (77kb)	Amedeo P et al. (2000) <i>Nature</i> 405(6783), 203-206
192	NADH-GOGAT (L01860)	plays a role in assimilation of symbiotically fixed N + role during pollen development	in nodules?	moderately chlorotic, reduced growth and reduced N-content + male sterility (=inviolate pollen); 50% transcript reduction	PAAT2 (nodule specific)-antisense-IE9	alfalfa ( <i>Medicago sativa</i> L.)	alfalfa ( <i>Medicago sativa</i> L.)	cDNA fragment (middle region) (2.5 kb)	Schoenbeck et al. (2000) <i>J Exp Bot</i> 51(342), 29-39
193	NADP-malate dehydrogenase	role in Photosynthesis?	?	yellow leaves (sometimes mosaic phenotype)	p7-antisense-	<i>Flaveria bidentis</i> L.	<i>Flaveria bidentis</i> L. (?)		Trevanion SJ et al. (1999) <i>Aust J Plant Physiol</i> 28, 537-547

	A	B	C	D	E	F	G	H	I
194	NAG1 (agamous)	floral identity gene (a putative AG gene)	flowers	floral aberrations; no RNA data...	p35S-sense-; p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment encoding the entire coding region (+0.7kb)	Kempin SA et al. (1993) Plant Physiol 103, 1041-1046
195	Napin	storage protein	seeds	reduced amounts of napin in seeds (no accumulation possible) change in fatty acid composition	napin promoter - antisense-nos terminator	Brassica <i>napus</i>	Brassica <i>napus</i>	cDNA fragment encoding the entire coding region (-0.7kb)	Khono-Murase et al. (1994) Plant Mol Biol 26(4), 1115-1124
196	Nia (nitrate reductase) and Nii (nitrit reductase) and promoters	stand for the reduction of nitrate into ammonium and the introduction of ammonium into the carbon skeleton provided by photosynthesis	cytosol for nitrate reductase; chloroplast for nitrite reductase	cell-autonomous chlorotic phenotype	p35S-sense or antisense-	<i>Nicotianae</i> species ( <i>Nicotiana tabacum</i> L. Or <i>N. plumbaginifolia</i> e)	<i>Nicotianae</i> species	endogenous Nia or Nii genes	Vaucheret et al. (1997) Euphytica 00, 195-200
197	nia (nitrate reductase)	Nitrate reduction	leaf	chlorosis; bleaching	p35S-sense-35S terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length cDNA (??kb) or cDNA fragments (bp)	Dorhac de Borne F et al. (1994) Mol Gen Genet 243, 613-621; Vaucheret H and Caboche M (1995) Plant Science 107, 95-104; Palauqui J-C and Vaucheret H (1995) Plant Mol Biol 29, 149-159; Vaucheret H et al. (1996) Plant Cell 9, 1495-1504; J-C Palauqui et al. (1997) EMBO J. 16(15), 4738-4745; Vaucheret H et al. (1997) Euphytica 00, 195-200; Palauqui J-C and Vaucheret H (1998) Proc Natl Acad Sci USA 95, 9675-9680
198	nicotianamine synthase	role in iron homeostasis (acid nicotianamine biosynthesis)	?	chlorosis of the leaf nervae	p??-antisense-	tobacco ( <i>Nicotiana tabacum</i> L.)	barley roots		Herbik A et al. (1999) Eur J Biochem 265(1), 231-239
199	Nii (nitrite reductase = NIR)	Nitrate reduction	leaf	chlorosis	p35S(2x)-sense nos terminator; p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment (1.85kb) or genomic DNA (4.5kb; 5.6kb)	Vaucheret H et al (1992) Plant J 2, 559-569; Vaucheret H et al. (1995) Mol Gen Genet 248(3), 311-307; Thierry and Vaucheret (1996) Plant Mol Biol 32(6), 1075-1083; J-C Palauqui et al. (1997) EMBO J. 16, 4738-4745; Vaucheret H et al. (1997) Euphytica 00, 195-200; Crete and Vaucheret (1999) Plant Mol Biol 41(1), 105-114
200	NR (Never-ripe)	Fruit ripening: ethylene receptor ("receptor inhibition" mode of action)	fruits	restoration of normal ripening (inhibition of the mutant Nr-gene)	p35S-antisense 35S terminator	tomato ( <i>Lycopersicon esculentum</i> )	tomato ( <i>Lycopersicon esculentum</i> )	cDNA fragment (714bp)	Hackett RM et al. (2000) Plant physiology 124, 1079-1085
201	ANRT1:2 (Arabidopsis CH1 gene)	role in constitutive low-affinity nitrate uptake.	root hairs and root epidermis	enhanced resistance to chlorate	p35S-antisense nos terminator	Arabidopsis <i>thaliana</i> L.	Arabidopsis <i>thaliana</i> L.	5'cDNA fragment (1.5kb)	Huang NC et al. (1999) Plant Cell 11(8), 1381-1392
202	class I OMT (o-methyl transferase)	lignin biosynthesis	lignified tissues (OMT I) or upon infection (OMT II)	modified lignin composition	p35S sense; p35S a.s.	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	range of cDNA fragments : full length (1457bp) to 300bp	Alanassova et al. (submitted EMBO 1995); Alanassova R et al. (1995) Plant J 8, 465-477
203	o-methyl transferase (b-OMT) - Ptomt gene	lignin biosynthesis	woody tissues	altered lignin composition	p35S-antisense 35S-terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	aspen ( <i>Populus</i> sp.) (Ptomt gene)	5'cDNA fragment (0.47kb)	Dwivedi UN et al. (1994) Plant Mol Biol 26(1), 61-71
204	Osmotine-like gene	role in plant defense	?	decrease in mRNA	p35S-antisense	potato ( <i>Solanum commersonii</i> Dun.)			Zhu B et al. (1996) Planta 198(1), 70-77
205	P5CS (1-pyrroline-5-carboxylate synthetase)	proline synthesis; role in osmotic stress	induced expression by dehydration, high salt and ABA treatment	morphologica alterations in leaves and a defect in elongation of inflorescences and hypersensitivity of leaves to osmotic stress	p35S-antisense GUS-nos terminator	Arabidopsis <i>thaliana</i> L.	Arabidopsis <i>thaliana</i> L.	cDNA (2584bp)	Nanjo T et al. (1999) Plant J 18(2), 185-193
206	PAI 1 (phosphoribosyl branilate isomerase)	tryptophan biosynthesis	???	blue fluorescence under UV light and resistance to the antranilate analog 6-methylanthranilate	p35S-antisense	Arabidopsis <i>thaliana</i> L.	Arabidopsis <i>thaliana</i> L.	cDNA fragment (0.8kb)	Li et al. (1995) Plant Cell 7(4):447-61;
207	AIPDHK (pyruvate dehydrogenase kinase)	negative regulator of the mitochondrial pyruvate dehydrogenase complex (miPDC)	all tissues	marked elevation of miPDC activity; altered vegetative growth with reduced accumulation of vegetative tissues, early flowering and shorter generation time	p35S-(dend)-antisense-	Arabidopsis <i>thaliana</i> L. (ecotype Columbia)	Arabidopsis <i>thaliana</i>	"internal" cDNA fragment (0.5kb)	Zou J et al. (1999) Plant Mol Biol 41(6), 837-849
208	PDS (phytoene desaturase)	carotenoid biosynthetic pathway	green leaves	white phenotype and phytoene accumulation	VIGS: pTMV U1-antisense- or pTMV U1-sense	<i>Nicotiana benthamiana</i>	tomato ( <i>Lycopersicon esculentum</i> Mill.)	cDNA fragment (648bp??)	Kumagai MH et al. (1995) Proc Natl Acad Sci USA 92(5), 1879-1883
209	PDS (phytoene desaturase)	photosynthetic pigment biosynthesis	green leaves	photobleaching	VIGS: p35S-sense-nos terminator or p35S-antisense-nos terminator	<i>Nicotiana benthamiana</i>	<i>Nicotiana benthamiana</i>	different cDNA fragment (415bp = central region)	Ruiz MT et al. (1998) Plant Cell 10(6), 937-946; Voinnet O et al. (2000) Cell 103, 157-167

	A	B	C	D	E	F	G	H	I
210	PE (pectin esterase)	role in pectin de-esterification	fruit	reduced enzyme activity; inhibition of mRNA accumulation; heavy pectin esterification	p35S-antisense nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill cv. Ailsa Craig)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	5'cDNA fragment (420bp)	Hall LN et al. (1993) <i>Plant J</i> 3(1), 121-129
211	PEPC (sppc) (Phosphoenol pyruvate carboxylase)	important role in primary photosynthetic CO <sub>2</sub> fixation in C4 and CAM plants	strongly regulated	decrease in malate levels; delayed stomatal opening	p35S-antisense	<i>Solanum tuberosum</i> L.	<i>Solanum tuberosum</i> L.	cDNA fragment (3094bp)	Gehlen J et al. (1996) <i>Plant Mol Biol</i> 32(5), 831-848
212	PFN (profilin)	actin-binding protein involved in the organization of the cytoskeleton	root and root hair; vascular bundles of cotyledons and leaves	stunted growth - dwarf phenotype - short hypocotyls	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment: coding region (3094bp)	Ramachandran S et al. (2000) <i>Plant Physiol</i> 124, 1637-1647
213	PFP (pyrophosphate: fructose-6-phosphate 1-phosphotransferase)	catalysis the conversion of fructose-6-phosphate and inorganic pyrophosphate to fructose-1,6-biphosphate and inorganic phosphate	ubiquitous	reduced activity of PFP in leaves: 58-95% in the leaf base and 87-97% at the leaf tip in T3 transformants; indication for changes in metabolic fluxes in leaves; (PFP regulation at the protein level...?)	p35S-antisense or sense-	tobacco ( <i>Nicotiana tabacum</i> L. cv. Samsun)	potato ( <i>Solanum tuberosum</i> L.); alfa PFP subunit	? (7bp)	Paul M et al. (1995) <i>Planta</i> 196(), 277-283; Nielsen TH and Stitt M (2001) <i>Planta</i> 214, 106-116
214	PG (poly-galacturonase = pTOM6; EC 3.2.1.15)	cell wall degradation, fruit ripening: pectin depolymerisation	fruit tissue	inhibition of fruit ripening	p35S-antisense-nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill cv. Ailsa Craig)	5'cDNA fragment (730bp; 50bp non coding r)	Smith CJS et al. (1988) <i>Nature</i> 334, 724-726; Schuch et al. (1989) <i>Plant Mol Biol</i> 13(3), 303-311; Smith CJS et al. (1990) <i>Plant Mol Biol</i> 14, 369-379; Gray et al (1992) <i>PMB</i> 19, 69-87
215	PG (poly-galacturonase)	cell wall degradation, fruit ripening: pectin depolymerisation	expressed only during the ripening stage of fruit development	downregulation of PG transcription in ripening fruits and reduction of PG activity	p35S-antisense-Tr 7 terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	cDNA (1624bp - complete ORF)	Sheehy RE et al. (1998) <i>Proc Natl Acad Sci USA</i> 85, 8805-8809
216	PG and PE	cell wall degradation, fruit ripening: pectin depolymerisation	fruit tissue	inhibition of fruit ripening	p35S-sense chimeric construct-35S terminator	tomato ( <i>Lycopersicon esculentum</i> Mill cv. Ailsa Craig)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	cDNA-fragments (244bp PG - 1320bp PE)	Seymour et al. (1993) <i>Plant Mol Biol</i> 23(1), 1-9
217	PG (poly-galacturonase)	cell wall degradation, fruit ripening: pectin depolymerisation	fruit tissue	inhibition of fruit ripening	p35S-antisense-nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	?	cDNA fragment (1500bp)	Ju R et al. (1994) <i>Chin J Biotechnol</i> 10(2), 67-74
218	PG1-beta subunit	cell wall degradation, fruit ripening: pectin depolymerisation	fruit tissue	increased levels of pectin solubilization and depolymerization during fruit ripening	p35S-antisense ?? Terminator (pBI121 vector)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	cDNA fragment (1790bp/2 227bp)	Watson CF et al. (1994) <i>Plant Cell</i> 6, 1623-1634
219	StpPGM (plastidial phosphoglucomutase; AJ420053)	starch biosynthesis	constitutive expression	decrease of starch accumulation and significant increase of sucrose and hexose phosphates	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (2.4kb)	Tauberger et al. (2000) <i>Plant J</i> 23(1), 43-53
220	PHA1 and PHA2 (P-type ATPase genes)	proton translocation machinery: ion and metabolite transport	depending on the isophorms	no transformants obtained	p35S-antisense	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (956-952 bp respectively)	Harms K et al. (1994) <i>Plant Mol Biol</i> 26(3), 979-988
221	Pho2 (cytosolic phosphotyrosyl)	possible influence on sprouting and flowering	leaves and tubers	changes in sprouting, flowering time and tuber yield	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	potato ( <i>Solanum tuberosum</i> L.)	cDNA (2kb)	Duweering E et al. (1997) <i>Plant J</i> 12(2), 323-333
222	10kd protein of the water splitting apparatus of photosystem II	photosynthesis	photosynthetically active cells	reduces protein and RNA amounts (significant) - retarded oxidation of QA + disorder in PSII complex	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (700bp)	Stockhous J et al. (1990) <i>EMBO J</i> 9(9), 3013-3021
223	PHYA (phytochrome A)	perception of light signals: role in the circadian clock	green tissues	less sensitive to red light with regard to stem elongation	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (3600bp) or internal cDNA frag (782bp)	Heyer AG et al. (1995) <i>Plant physiol</i> 109(1), 53-61; Yanovsky MJ et al. (2000) <i>Plant J</i> 23(2), 223-232
224	PHYB (phytochrome B)	perception of light signals: role in the circadian clock	green tissues	elongated stems and reduced chlorophyll content; photoperiodic control of fiberization	p35S-antisense	<i>Solanum tuberosum</i> L. ssp. <i>andigena</i>	potato ( <i>Solanum tuberosum</i> L.)	cDNA fragment (1300bp)	Jackson SD et al. (1996) <i>Plant J</i> 9(2), 159-168; Yanovsky MJ et al. (2000) <i>Plant J</i> 23(2), 223-232
225	PIF3 (phytochrome interacting factor)	phytochrome signalling (control of gene expression?)	?	perturbation of photoresponsiveness	p35S-antisense 35S-terminator	<i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>	cDNA fragment - ORF (1.6kb)	Ni M et al. (1998) <i>Cell</i> 95(5), 657-667
226	Plastid aldolase	calvin cycle	leaves	marked consequences for photosynthesis, carbon partitioning and growth	p35S-antisense ocs terminator	<i>Solanum tuberosum</i> L. cv Désirée	<i>Solanum tuberosum</i> L.	full-length cDNA (1270bp)	Haake et al. (1998) <i>Plant J</i> 14(2), 147-157

	A	B	C	D	E	F	G	H	I
227	PLD (phospholipase D; EC 3.1.4.4)	role in membrane deterioration; a phospholipid hydrolyzing enzyme	?	slower rate of leaf senescence	p35S-antisense rbcS terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (261bp)	Fan L et al. (1997) <i>Plant Cell</i> 9(12), 2183-2196
228	PMA (plasma membrane H <sup>+</sup> -ATPase)	proton translocation in plasma membranes; ion and metabolite transport	depending on the isophorms	reduction of transcript	antisense	various higher plants			Perez and Boutry (1994) <i>Symp Soc Exp Biol</i> 48,11-22
229	PME (pectin methyl esterase)	pectin demethylation	constitutive expression	root development?	p35S-sense- rbcS terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	genomic DNA: 1.6kb	Mishra and Handa (1998) <i>Plant Journal</i> 14, 583-592
230	PME (pectin methyl esterase; EC 3.1.1.11)	cell wall degradation, fruit ripening; regulation of methanol biosynthesis	fruit tissue	inhibition of fruit ripening	p35S-sense- rbcS terminator; p35S-antisense rbcS terminator	tomato ( <i>Lycopersicon esculentum</i> Mill. Cv. Rutgers)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	genomic DNA: 1.6kb	Tieman et al (1992) <i>Plant Cell</i> 4, 667-679; Gaffa J et al (1997) <i>Plant Physiol</i> 114(4), 1547-56; Frenkel C (1998) <i>J Biol Chem</i> 273(8), 4293-4295
231	PME (pectin methylesterase) and polygalacturonase	enzymes of the pectin degradation pathway	fruits	significant downregulation of both genes	antisense PME - antisense polygalacturonase	tomato ( <i>Lycopersicon esculentum</i> )			Pear JR et al. (1993) <i>Antisense Res Dev</i> 3(2), 181-190
232	rcPME1 (pectin methylesterase)	maintenance of extracellular pH, elongation of cells within the root tip, and cell wall degradation	periferal cells of the root cap	prevention of the normal separation of root border cells from the root tip	p35S-sense-; p35S-antisense (vector pBI121)	pea ( <i>Pisum sativum</i> cv. Little Marvel)	pea ( <i>Pisum sativum</i> cv. Little Marvel)	cDNA: 1744bp	Wen F et al. (1999) <i>Plant Cell</i> 11(6), 1129-1140
233	PORA or PORB (light dependent NADPH:Phlide oxidoreductases)	catalyzed of the only light-dependent reaction in the chlorophyl biosynthetic pathway	green tissues	antisense: 2 to 10-fold decrease of transcript and 2 to 3 fold decrease of protein; changed plastid architecture	p35S + omega enhancer- antisense-	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA: complete coding region (7kb)	Franck F et al. (2000) <i>Plant Physiol</i> 124, 1678-1696
234	PPO (polyphenol oxidase)	first step in the synthesis of polyphenols (melanin)	ubiquitous	tolerance of tubers against bruising = black spot resistance	p35S-antisense nos terminator; pGBSS-antisense-nos terminator; pPATATIN-antisense-nos terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	full-length or 5'frag cDNA: 1875bp (class I) - 1931bp (class II) or 800bp frg.	Bachem CWB et al. (1994) <i>Nature Bio/technology</i> 12, 1101-1105
235	PPO (polyphenol oxidase)	first step in the synthesis of polyphenols (melanin)	??	repressed PPO activity; lower browning potential of the fruit	p??-antisense-	apple			Murata M et al. (2000) <i>J Agric Food Chem</i> 48(11), 5243-5248
236	P-protein (small subunit of GDC)	glycine breakdown	ubiquitous	decrease in the ability of the leaf mitochondria to decarboxylate glycine; reduced photosynthetic and growth rates	PST-LS1- antisense-locs	potato ( <i>Solanum tuberosum</i> L. cv. Desiré)	potato ( <i>Solanum tuberosum</i> L.)	full-length cDNA (2.4kb)	Heineke D et al. (2001) <i>Planta</i> 212(5/6), 880-887
237	PRK (Phosphoribulokinase)	calvin cycle	green tissues	reduced amounts of hexose and starch; lower CO <sub>2</sub> assimilation; reduced relative growth rate of shoots and delayed flowering - resistance to <i>P. parasitica</i>	PrbcS- antisense-nos terminator	Tobacco ( <i>Nicotiana tabacum</i> L.)	Tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment (1.3kb)	Paul MJ et al. (1995) <i>Plant J</i> 7(4), 535-542
238	AtProDH (proline dehydrogenase; ERD5 sequence; D83025)	role in proline degradation	drought-inducible gene	proline accumulation, enhanced stress tolerance	P35S-antisense GUS-nos (in pBE2113)	<i>Arabidopsis thaliana</i> (L.) Heynh. ecotype Columbia	<i>Arabidopsis thaliana</i> (L.) Heynh.	full-length cDNA (1.85kb)	Nanjo T et al. (1999) <i>FEBS Lett</i> 461(3), 205-210
239	prosystemin (systemin precursor gene)	precursor of systemic wound signal	all tissues but not in roots; wound inducible	greatly suppressed systemic wound induction of proteinase inhibitor I and II synthesis	P35S-antisense	tomato ( <i>Lycopersicon esculentum</i> Mill.)	Lycopersicon esculentum Mill.)	cDNA fragment (747bp)	McGurl B et al. (1992) <i>Science</i> 255, 1570-1573; Orozco-Cardenas and Ryan (1999) <i>Proc Natl Acad Sci USA</i> 96(11), 6553-6557; Narvaez-Vasquez J et al. (1999) <i>Plant Cell</i> 11(11), 2249-2260
240	psbW	putative crucial role in biogenesis and regulation of the photosystem apparatus; subunit of PSII	green tissues	lack of dimeric PSII supraplex; decreased oxygen-evolving rate, low psbW mRNA	p35S-antisense (pBin19)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	genomic DNA fragment (??kb)	Shi LX et al. (2000) <i>J Biol Chem</i> 275(48), 37945-37950
241	PSI-F (psaF clone)	a subunit of the photosystem I (PSI)	green tissues	lethal, stunted growth in surviving plants	pE35S- antisense-35S terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length cDNA (664bp)	Haldrup A et al. (2000) <i>J Biol Chem</i> 275(40), 31211-31218
242	PSI-H	a subunit of the photosystem I (PSI)	green tissue	smaller habitus when grown on sterile media; decrease of the proton gradient across the thylacoid membrane	p35S-sense- (pBIN121)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (??bp) - with entire coding region	Naver H et al. (1999) <i>J Biol Chem</i> 274(16), 10749-10789
243	PSI-K (psaK-cDNA)	a subunit of the photosystem I (PSI)	green tissue	higher chlorophyl a/b ratio, more P700 than WT	p35S-antisense 35S terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full length cDNA clone: 540bp	Jensen PE et al. (2000) <i>J Biol Chem</i> 275(32), 24701-24708

	A	B	C	D	E	F	G	H	I
244	PSI-N (psaN)	a subunit of the photosystem I (PSI)	protein located entirely in thylakoid lumen: green tissue	under sub-optimal conditions: chlorosis and slower growth; under optimal conditions: no phenotypic alterations but several photosynthetic parameters were affected	p35S-antisense- nos terminator and co-suppression: p35S-sense- 35S terminator	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	antisense: EST DNA fragment: 515bp; sense: full length cDNA: ??bp	Haldrup A et al. (1999) <i>Plant J</i> 17(6), 686-698
245	OsPSK (Oryza sativa Phytosulfokine-alpha)	PSK-alpha precursor: role in cell proliferation	?	60% reduction of PSK-alpha production compared to control level	pACTIN(rice) - antisense-	<i>Oryza sativa</i> L. (Oc cells)	<i>Oryza sativa</i> L. (Oc cells)	cDNA clone: 725bp?	Yang H et al. (1999) <i>Proc Natl Acad Sci USA</i> 96(23), 13560-13565; Yang H et al. (2000) <i>Plant Cell Physiol</i> 41(8), 811-816
246	pyruvate, orthophosphate dikinase	role in Photosynthesis?	?	yellow leaves (sometimes mosaic phenotype)	p7-antisense-	<i>Flaveria bidentis</i> L.	<i>Flaveria bidentis</i> L. (?)		Trevanion SJ et al. (1999) <i>Aust J Plant Physiol</i> 26, 537-547
247	phytene synthase (Psy1) = TOM5	carotenoid lycopene biosynthesis	ripening fruit	inhibition of carotenoid production in ripening fruit; yellow fruit; pale flowers	p35S-antisense- nos terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	5'cDNA fragment (794bp)	Bird CR et al. (1991) <i>Nature Biotechnology</i> 9(7), 635-639; Bramley et al. (1992) <i>Plant J</i> 2(3), 343-349; Fraser PD et al. (1999) <i>Plant Mol Biol</i> 40(4), 687-698
248	phytene synthase (Psy1) = TOM5	carotenoid lycopene biosynthesis	ripening fruit	inhibition of carotenoid production in ripening fruit; susceptibility to photobleaching in leaves (other Psy??); yellow fruit; white flowers	p35S-sense- 35S terminator	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	functional cDNA (1455bp)	Fray and Grierson (1993) <i>PMB</i> 22, 589-602
249	AIPTR2-B	peptide transport gene (role in plant nutrition?)	constitutively expressed in all plant organs	reduction of mRNA - in leaves and flowers (not in roots). Late flowering and arrested seed development	p35S-sense-??- or p35S- antisense-??	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (+/- 1.65kb)	Song et al. (1997) <i>Plant Physiol</i> 114(3), 927-935
250	RA14-like: 16kDa Allergenic proteins	allergenic compounds found in seeds	seeds	lower amounts of allergenic compounds in seeds (=Immunoblot and RNA-blot analysis)	rice allergenic promoter - antisense- twaxy**; rice seed-specific promoters - antisense+ antisense (or +sense)- twaxy**	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)	genomic DNA (bp)	Nakamura R and Matsuda T (1996) <i>Biosci Biotechnol Biochem</i> 60(8), 1215-1221
251	RA17: 14-16kDa Allergenic proteins	allergenic compounds found in seeds	seeds	lower amounts of allergenic compounds in seeds (=Immunoblot and RNA-blot analysis)	rice seed-specific promoters - antisense- twaxy**	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)	cDNA (550bp)	Tada Y et al. (1996) <i>FEBS Lett</i> 391(3), 341-345;
252	MsRAC1 (a GTP-binding protein)	role in the establishment of plant defence reactions	"ubiquitously expressed in various tissues"	poor growth and retarded flowering	p35S-antisense- nos-	tobacco ( <i>Nicotiana tabacum</i> L.)	alfalfa ( <i>Medicago sativa</i> )	cDNA, coding region (593bp)	Schiene K et al. (2000) <i>Mol Gen Genet</i> 263(5), 761-770
253	3RT (anthocyanin-3-glucoside: rhamnosyltransferase)	pigment gene	flowers	interference with the production of malvidin: accumulation of delphinidin-3 glucosides; lighter coloured flowers	pMac-antisense	<i>Petunia hybrida</i>	<i>Petunia hybrida</i>	cDNA fragment (1.7kb)	Brugliera F et al. (1994) <i>Plant J</i> 5(1), 81-92
254	Rac13 (GTPase)	role in H2O2 production (activation of NADPH oxidase) and cell wall formation	highly induced expression at the transition from primary to secondary wall synthesis	decreased levels of H2O2 upon cell wall formation	p35S-antisense	soybean ( <i>Glycine max</i> ) and <i>Arabidopsis thaliana</i> L. cells	cotton ( <i>Gossypium hirsutum</i> )		Potikh TS et al. (1999) <i>Plant Physiol</i> 119(3), 849-858
255	rbcS (Rubisco, small subunit)	small subunit of ribulose bisphosphate carboxylase; calvin cycle	photosynthetic eucaryotic cells	yellow-green chlorosis in and around the veins of systemic leaves	VIGS: p35S-sense- nos terminator	<i>Nicotiana benthamiana</i>	<i>Nicotiana benthamiana</i>	cDNA fragment (0.5kb)	Jones L et al. (1998) <i>Plant Cell</i> 11(12), 2291-2301; Voinnet et al (2000) <i>Cell</i> 103, 157-167 (see PDS)
256	rbcS (Rubisco, small subunit)	small subunit of ribulose bisphosphate carboxylase; calvin cycle	photosynthetic eucaryotic cells	decrease in RUBISCO activity; significant reduction in carbonic anhydrase activity; decrease in photosynthesis	p35S-antisense- nos terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment (0.6kb)	Hudson GS et al. (1992) <i>Plant Physiol</i> 98(1), 294-302
257	rbcS (Rubisco, small subunit)	small subunit of ribulose bisphosphate carboxylase; calvin cycle	photosynthetic eucaryotic cells	80% mRNA reduction; 85% protein reduction; stunted growth	p35S-antisense- 35S-terminator	<i>Flaveria bidentis</i> L.	<i>Flaveria bidentis</i> L.	full-length cDNA clone (689bp)	Furbank RT et al. (1998) <i>Plant Physiol</i> 111(3); 725-734; Maroco JP et al. (1998) <i>Plant Physiol</i> 116(2), 823-832
258	rbcS (Rubisco, small subunit)	small subunit of ribulose bisphosphate carboxylase; calvin cycle	photosynthetic eucaryotic cells	reduction in transcription levels (40%) and smaller biomass when grown in 36Pa CO2 (normal CO2 content)	PrbcS- antisense-nos	rice ( <i>Oryza sativa</i> L.)	rice ( <i>Oryza sativa</i> L.)	cDNA fragment (819bp)	Makino A et al. (1997) <i>Plant Physiol</i> 114, 483-491; Makino A et al. (2000) <i>Aust J Plant Physiol</i> 27, 1-12; Makino A et al. (2000) <i>J Exp Bot</i> 51(Spec No), 383-399
259	rbcS (Rubisco, small subunit)	small subunit of ribulose bisphosphate carboxylase; calvin cycle	photosynthetic eucaryotic cells	reduced levels of rbcS mRNA; striking variations in growth that are correlated with antisense gene dosage	p35S-antisense- 35S terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	<i>Nicotiana sylvestris</i>	5'cDNA fragment (321bp)	Rodermeier et al (1998) <i>Cell</i> 55(4), 673-681; Quick WP et al. (1992) <i>Planta</i> 188, 522-531; Jiang CZ et al. (1994) <i>Plant Mol Biol</i> 25(3), 569-576; Rodermeier et al. (1996) <i>Proc Natl Acad Sci U S A</i> , 93(9):3881-3885
260	Rieske FeS protein	role in photosynthesis	?	reduction (<10%) in transcription levels	35S-antisense-	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	5'cDNA fragment (321bp)	Palomares R et al. (1993) <i>Planta</i> 190(3), 305-312; Price GD et al. (1995) <i>Aust J Plant Physiol</i> 22, 285-297; Price GD et al. (1998) <i>Aust J Plant Physiol</i> 25, 445-452
261	Rep1AI (pollen specific Rop GTPase)	key molecular switch controlling tip growth in At pollen tubes	pollen?	Inhibited pollen-tube growth at 0.5mM extracellular Ca(2+)	pLAT52 (pollen-specific)- antisense-	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	full-length cDNA clone (630bp??)	Li H et al. (1999) <i>Plant Cell</i> 11(9), 1731-1742
262	AI RP3A (histone deacetylase; AF195547)	role in gene repression (putative deacetylase gene)	leaves, stems, flowers and young siliques	decreased endogenous AI RP3A transcript and delayed flowering	p-394TCUP-truncated antisense-	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (519bp)	Wu K et al. (2000) <i>Plant Mol Biol</i> 44, 167-176
263	Rca (Rubisco activase)	Rubisco activation <i>in vivo</i>	photosynthetic eucaryotic cells???????????	reduction in transcript level and influence on steady state photosynthesis	35S-antisense- nos terminator	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L. cv. W38)	3'cDNA fragment (1.2kb; 1.1kb)	Mate CJ et al. (1993) 102(8), 1119-1128; Jiang CZ et al. (1994) <i>Plant J</i> 5(6), 787-798; Mate CJ et al. (1996) <i>Planta</i> 198, 804-813; Hammond ET et al. (1998) <i>Plant J</i> 14(1), 101-110

	A	B	C	D	E	F	G	H	I
264	at2S2 (2S-albumin)	Seed storage protein	seed	reduction of albumin amounts in seeds; enhanced expression of co-introduced gene	<i>Parc5-1</i> - antisense-tarc5-1	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	fragment (571bp)	Goossens et al. (1999) FEBS lett 456(1), 160-164
265	S3 (S-protein)	role in gametophytic self-incompatibility; a ribonuclease	pistil-specific	loss of S3 and S2 incompatibility	pS3-antisense-nos terminator	<i>Petunia inflata</i> (S2S3-genotype)	<i>Petunia inflata</i>	cDNA fragment; 70% of full length (585bp)	Lee H-S et al. (1994) Nature 367(6463), 560-563
266	S-64 (sucrose binding protein - SBP- homologue)	important component of the sucrose translocation	??	reduction in plant growth and development; decreased photosynthesis...	p35S-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	soybean ()		Pedra JHF et al. (2000) Plant Science 152(1), 87-98
267	SA2-Rnase (a ribonuclease)	ribonuclease = Altel-specific pollen rejection (self incompatibility)	predominantly in mature pistils	low SA2 transcript level = pollen acceptance	p35S(2xEnh)-antisense-tbos; pChIP-antisense-tbos; pRNA(soybean) antisense-	<i>Nicotiana alata</i> * <i>Nicotiana plumbaginifolia</i>	<i>Nicotiana alata</i>	cDNA fragment (550bp)	Murfett J et al. (1995) Plant Mol Biol 29(2), 201-212
268	SAHH (S-adenosyl-L-homocysteine hydrolase; EC 3.3.1.1)	key enzyme in the regulation of intracellular methylation reactions	?	distinct morphological changes: dwarfism, floral aberrations in stamen, wrinkled leaves with dark green colour	p35S-antisense (pBI121)	tobacco ( <i>Nicotiana tabacum</i> L. cv. BY-4 and Xanthi)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA (777bp)	Tanaka et al. (1997) Plant Mol Biol 35(6), 981-986
269	SAMDC (S-Adenosylmethionine decarboxylase; EC 4.1.1.50)	biosynthesis of the polyamines spermidine and spermine	increase of SAMDC activity during the early stages of polymerisation	decrease in SAMDC transcript level, SAMDC activity and total polyamine levels	patatin promoter antisense or sense- (pBIN19); p35S(2x)-antisense-i3SS or tetr inducible prom-antisense tocs	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	cDNA fragment (1600bp; 1800'7bp)	Kumar A et al. (1996) Plant J 9(2), 147-158; Pedros et al. (1999) Planta 209(1), 153-160
270	SBE A (starch branching enzyme)	role in starch biosynthesis	predominant in leaves	reduction in SBE A, altered tuber starch composition	p2*35S-antisense-nos terminator; pGBSS I-antisense...	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	cDNA fragment (1200bp)	Jobling SA et al. (1999) Plant J 18(2), 163-171
271	SCINVm (soluble acid invertase)	role in sucrose degradation	?	moderate invertase inhibition and increased sucrose accumulation	p7-antisense-	sugarcane ( <i>Saccharum officinarum</i> L.) - callus	sugarcane ( <i>Saccharum officinarum</i> L.)		Ma H et al. (2000) Aust J Plant Physiol 27,1021-1030
272	SHL (short life; H37427)	novel putative regulator of gene expression (contains a BAH domain and a PHD finger)	predominant expression in roots, stems, rosette leaves, cauline leaves and flowers	dwarfism and delayed development	p35S-antisense tocs (pBINAR)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragment (1100bp)	Mussig C et al. (2000) Mol Gen Genet 264(4), 363-370
273	AI SK11 (ASK-alpha) and AI SK12 (ASK-gamma)	role in the flower organ patterning (SHAGGY-related protein kinases)	flower meristems	flower aberration	p35S-antisense	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	5' extremity of the genes (+/- 300bp)	Domeias MC et al. (2000) Plant J 21(5), 419-429
274	SLG6	implicated in the self-incompatibility response	stigma tapetum and microspores	breakdown of self-incompatibility	p35S (truncated) SLG6-antisense-tbos	<i>Brassica rapa</i>	<i>Brassica rapa</i>	cDNA fragment (1.5kb)	Shiba H. et al. (2000) Biosci Biotechnol Biochem. 64(5):1016-24.
275	SLR1 (SLG-like receptor 1)	adhesive function in the pollination process	papillar cells of <i>Brassica</i> stigmas	altered kinetics of pollen adhesion, reduced levels of SLR1 glycoprotein and reduced transcript	p7-antisense-	<i>Brassica napus</i> cv. Westar	<i>Brassica</i> spp.		Franklin TM et al. (1996) Sex. Plant Reprod 9(4), 203-208; Luu DT et al. (1999) Plant Cell 11(2), 251-262
276	StSNAP	hypothetical function in vesical targeting and fusion during plant development	expressed in actively dividing tissues	altered morphology such as curled leaf, alteration in cellular development and assimilate distribution	pGBSS-antisense; p35S-antisense	<i>Solanum tuberosum</i> L. cv. Karmico	<i>Solanum tuberosum</i> L.	cDNA fragment (897bp)	Bachem CWB et al. (2000) Plant Mol Biol 43(4), 473-482
277	stylar SP41 alpha	beta-1,3-glucanase activity	stylus	no detection possible of gene of interest via enzymological and immunological tests	p35S-omega enhancer-antisense-tbos	<i>tobacco</i> ( <i>Nicotiana tabacum</i> L. cv. Samsun NN)	<i>tobacco</i> ( <i>Nicotiana tabacum</i> L. cv. Samsun NN)	cDNA fragment (5' of coding sequence) - 722bp	Sessa G and Fluhr R et al. (1995) Plant Mol Biol 29(5), 969-982
278	SP (self-pruning)	regulation of the alteration between vegetative and reproductive cycles in sympodial meristems	early stage from shoot apices and leaves and later floral primordia	indeterminate phenotype	p35S-antisense	<i>tomato</i> ( <i>Lycopersicon esculentum</i> Mill.)	<i>tomato</i> ( <i>Lycopersicon esculentum</i> Mill.)	cDNA (777kb)	Pnueli L et al. (1998) Development 125(11), 1979-1989
279	SPS (sucrose phosphate synthase; EC 2.4.7.14) and cFBPase	photosynthetic carbon metabolism	tubers	inhibition of sucrose synthesis and increase of starch	p35S-antisense and sense-	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	cDNA fragments (as; coding sequence: 3.4kb; sense: 2.0kb)	Geigenberger P et al. (1999) Plant J 19(2): 119-129
280	SPS (sucrose phosphate synthase; EC 2.4.7.14) and cFBPase	photosynthetic carbon metabolism	leaves	inhibition of sucrose synthesis ...	p35S-antisense nos	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	ESTs: SPS: 1810bp 5' part; cFBPase: 1060bp full length	Strand et al. (2000) Plant J 23(6), 759-770
281	SSI or SSII	starch biosynthesis	sink and source leaves	reduction of enzyme	p35S-antisense ocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	cDNAs: SSI: 1700bp 5' part; SSII: 1900bp 5' part	Kossmann et al. (1999) Planta 208(4), 503-511
282	SSIII	starch biosynthesis	tubers	profound change in the morphology of starch granules	p35S(2x)-antisense-i3SS (pBIN19)	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	5' cDNA fragment: 1100bp	Marschall J et al. (1998) Plant Cell 8, 1121-1135

	A	B	C	D	E	F	G	H	I
283	SSIII	starch biosynthesis	tubers, sink and source leaves	drastic change in granule morphology, increased level of covalently linked phosphate	p35S-antisenseocs terminator	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L. cv. Désirée)	5' cDNA fragment: 2300bp	Abel et al (1996) Plant J 10(6), 981-991; Lloyd et al. (1999) Biochem J 338 (Pt2), 515-521
284	stearoyl-ACP-desaturase (=stearoyl-acyl carrier protein desaturase EC 1.14.99.6)	catalyzes the first desaturation step in seed oil biosynthesis	in developing rape seed embryos	increased stearate levels in the seeds	pB.rapeNAPIN-antisense-trapin + pB.rapeACP-antisense-tACP	<i>Brassica rapa</i> cv. Tobin; <i>Brassica napus</i> cv. A112	<i>Brassica rapa</i> cv. R500	cDNA fragment: 1160bp	Knutson DS et al. (1992) Proc Natl Acad Sci USA 89(7), 2624-2628
285	sucrose synthase (L19762)	sucrose hydrolysis	fruits	no influence on starch or sugar accumulation'	p2A11 - antisense-inos	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill. cv. Moneymaker)	cDNA fragment: 2600bp	Chengappa S et al. (1999) Plant Mol Biol 40(2), 213-221
286	sucrose synthase (X75332)	determinant of plant growth: sucrose feeding into metabolism	overall	markedly smaller roots and leaves: suggesting major role in plant growth	p35S-antisenseinos (pBI121)	carrot ( <i>Daucus carota</i> L.)	carrot ( <i>Daucus carota</i> L.)	cDNA fragment: 2134bp	Tang GQ and Sturm A (1999) Plant Mol Biol 41(4), 465-479
287	Susy (sucrose synthase)	sucrose cleavage	sink tuber	strong accumulation of reducing sugars and inhibition of starch accumulation in developing tubers	p35S-antisenseocs	potato ( <i>Solanum tuberosum</i> L.)	potato ( <i>Solanum tuberosum</i> L.)	cDNA fragment: 2440bp; coding region	Zrenner et al (1995) Plant J 7(1), 97-107
288	SuSy (sucrose synthase; L19762); TOMSSF (fruit specific SuSy)	participates in the control of sucrose import capacity of young tomato fruit	flowers and fruit pericarp	reduced fruit set and slower growth rate of the fruit	p35S-antisense (pBI121)	tomato ( <i>Lycopersicon esculentum</i> Mill.)	tomato ( <i>Lycopersicon esculentum</i> Mill. cv. Summerset)	cDNA fragment: 538bp	D'Aoust MA et al. (1999) Plant Cell 11(12), 2407-2418
289	NtSUT1 (H+-sucrose cotransporter)	translocation of sucrose from the mesophyll to the phloem	mature leaves	mRNA reduction, curled down leaves, chloroses, necroses and death	p35S-antisenseocs	tobacco ( <i>Nicotiana tabacum</i> L. cv SNN)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment: 1200bp	Burkler et al. (1998) Plant Physiol 118(1), 59-68
290	TDC (tryptophan decarboxylase; EC 4.1.1.28)	key step in the biosynthesis of terpenoid Indole alkaloids	in tumour calluses (transcriptionally induced by fungal elicitors)	decreased levels of TDC activity	p35S-antisensei35S	Madagascar periwinkle ( <i>Catharanthus roseus</i> )	Madagascar periwinkle ( <i>Catharanthus roseus</i> )	cDNA fragment: ??bp	Goddijn OJ et al. (1995) Transgenic Res 4(5), 315-323
291	TK (plastid transketolase; A52295; <i>Nt-TK-26</i> )	role in the Calvin cycle and the oxidative pentose phosphate pathway and formation of precursors to the shikimate and phenypropanoid metabolism	ubiquitous expression	bleaching	p35S-antisenseocs	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA fragment: 1282bp	Henkes S et al. (2001) Plant Cell 13(3), 535-551
292	TMS (tomato MADS box gene no. 5) and TM6	flower specific MADS box gene	expressed in primordial and developing stages of petals, stamens and gynoecia	flower aberrations	p35S-antisense (pBI121)	tomato ( <i>Lycopersicon esculentum</i> L.)	tomato ( <i>Lycopersicon esculentum</i> L.)	full-length cDNAs: TMS: 910bp ; TM6: 902bp	Pnueli L et al. (1994) Plant Cell 6(2), 175-186
293	atToc34 and atToc33	components of the chloroplast protein import machinery	overall but developmentally regulated	pale yellowish phenotype	p35S-antisense (pGTV-BAR vector)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA fragments : atToc34, 942bp; atToc33, 981bp	Gutensohn M et al. (2000) Plant J 23(6), 771-783
294	alphaTPT (chloroplast triose phosphate/phosphate translocator)	control on the flux of starch and sucrose biosynthesis, CO <sub>2</sub> assimilation, respiration and photosynthetic electron transport	green and non green tissue	In elevated CO <sub>2</sub> and low O <sub>2</sub> and saturating light conditions: increased 14C incorporation into starch;	p35S-antisensei35S (pBIN19)	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	cDNA clone: 1200bp	Häusler RE et al. (1998) Planta 204(3), 366-376; Häusler RE et al. (2000) Planta 210(3), 371-382; Häusler RE et al. (2000) Planta 210(3), 383-390
295	TPT (chloroplastic triosephosphate translocator)	translocation of sugars to the chloroplasts (Calvin cycle?)	?	retarded growth at early developmental stages	p35S-antisensei35S	<i>Solanum tuberosum</i> L. cv Désirée	<i>Solanum tuberosum</i> L.	cDNA fragment: 1350bp	Reismeier JW et al. (1993) Proc Natl Acad Sci USA 90, 6160-6164; Kauder F et al. (2000) J Exp Bot 51(Spec No), 429-437
296	TPX (lignin-forming peroxidase)	lignin biosynthesis???	?	TPX-mRNA reduction	p35S-antisense + 3S-ribozyme (R2) + tRNA-R2	tobacco ( <i>Nicotiana tabacum</i> L.)			McIntyre CL et al. (1996) Transgenic Res 5(4), 263-270
297	TRAMP	a ripening-associated membrane protein; putative aquaporin; role in movement of solutes between cell compartments	ripening fruit	94% reduction in transcript; marked alterations in the normal pattern of accumulation of both organic acids and sugars	p35S-antisensei35S; P2A11-antisense-i35S (both in pBIN19)	tomato ( <i>Lycopersicon esculentum</i> L. cv. Alisa Craig)	tomato ( <i>Lycopersicon esculentum</i> L.)	cDNA fragment: 760bp	Chen G et al. (2001) Planta 212(5/6), 799-807
298	TTS (TTS-2)	stimulation of pollen tube growth	flowers	reduction of pollen tube growth	p35S(2x)-sense ; TTS 1-antisense	tobacco ( <i>Nicotiana tabacum</i> L.)	tobacco ( <i>Nicotiana tabacum</i> L.)	full-length cDNA: 967bp?	Cheung AY et al. (1995) Cell 82(3), 383-393
299	UDP-Glc epimerase (Z54214)	catalysis of the reversible epimerization of UDP-galactose and UDP-glucose	?	repressed growth in galactose containing medium correlated with decreasing enzyme activity	p35S-antisense (pBINAR-Hyg)	<i>Arabidopsis thaliana</i> L.	<i>Arabidopsis thaliana</i> L.	cDNA clone: 1356bp	Dormann P and Benning C (1998) Plant J 13(5), 641-652

